#### SEQUENCE LISTING

#### (1) GENERAL INFORMATION:

- (i) APPLICANT: MAERTENS, GEERT
  BOSMAN, FONS
  DE MARTYNOFF, GUY
  BUYSE, MARIE-ANGE
- (ii) TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
- (iii) NUMBER OF SEQUENCES: 111
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: NIXON & VANDERHYE P.C.
    - (B) STREET: 1100 NORTH GLEBE ROAD
    - (C) CITY: ARLINGTON
    - (D) STATE: VIRGINIA
    - (E) COUNTRY: U.S.A.
    - (F) ZIP: 22201-4714
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/612,973
    - (B) FILING DATE: 11-MAR-1996
    - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: BYRNE, THOMAS E.
  - (B) REGISTRATION NUMBER: 32,205
  - (C) REFERENCE/DOCKET NUMBER: 1487-10
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (703) 816-4000
    - (B) TELEFAX: (703) 816-4100
- (2) INFORMATION FOR SEQ ID NO: 1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 21 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO

	Tyr	His	Val 35	Thr	Asn	Asp	Cys	Ser 40	Asn	Ser	Ser	Ile	Val 45	Tyr	Glu	Ala	
				ATC Ile													192
				TCC Ser													240
				AGC Ser													288
I.	Leu			GCG Ala 100													336
	TGC Cys	Gly	Ser 115	GTC Val	Phe	Leu	Val	Ser 120	Gln	Leu	Phe	Thr	Ile 125	Ser	Pro	Arg	384
	Arg	CAT His 130	GAG Glu	ACG Thr	GTG Val	CAG Gln	GAC Asp 135	TGC Cys	AAT Asn	TGC Cys	TCA Ser	ATC Ile 140	TAT Tyr	CCC Pro	GGC Gly	CAC His	432
in the second	<b>-</b> -			CAC His													480
	ACA Thr	ACG Thr	GCC Ala	CTG Leu	GTG Val 165	GTA Val	TCG Ser	CAG Gln	CTG Leu	CTC Leu 170	CGG Arg	ATC Ile	CCA Pro	CAA Gln	GCT Ala 175	GTC Val	528
				GTG Val 180													576
				ATG Met													624
		TTT Phe 210		CTC Leu	TAAT	rag											642
	(2)	INFO	ORMA1	rion	FOR	SEQ	ID N	10: 4	1:								
		(		SEQUE													
				3) TY 0) TO													
		(ii)	MOI	LECUI	LE TY	(PE:	prot	ein									
		(xi)	SE	QUENC	CE DE	ESCRI	PTIC	on: s	SEQ :	D NO	): 4:	:					
	Met 1	Pro	Gly	Cys	Ser 5	Phe	Ser	Ile	Phe	Leu 10	Leu	Ala	Leu	Leu	Ser 15	Cys	

Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg 120 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ille Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro <sub>=</sub> 145 150 Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val 170 Twal Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala 180

Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu 195 200 205

Leu Phe Ala Leu 210

#### (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 795 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
    (B) LOCATION: 1..792
- (ix) FEATURE:

(A) NAME/KEY: mat\_peptide (B) LOCATION: 1..789

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG Met 1	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACA Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
ACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192
ICTG LLeu 65	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240
TCC Ser																288
TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
CTC Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
GTC Val 145	GAT Asp	TTG Leu	CTC Leu	GTT Val	GGG Gly 150	GCG Ala	GCT Ala	GCT Ala	TTC Phe	TGT Cys 155	TCC Ser	GCT Ala	ATG Met	TAC Tyr	GTG Val 160	480
GGG Gly	GAC Asp	CTC Leu	TGC Cys	GGA Gly 165	TCT Ser	GTC Val	TTC Phe	CTC Leu	GTC Val 170	TCC Ser	CAG Gln	CTG Leu	TTC Phe	ACC Thr 175	ATC Ile	528
TCG Ser	CCT Pro	CGC Arg	CGG Arg 180	CAT His	GAG Glu	ACG Thr	GTG Val	CAG Gln 185	GAC Asp	TGC Cys	AAT Asn	TGC Cys	TCA Ser 190	ATC Ile	TAT Tyr	576
CCC Pro	GGC Gly	CAC His 195	ATA Ile	ACG Thr	GGT Gly	CAC His	CGT Arg 200	ATG Met	GCT Ala	TGG Trp	GAT Asp	ATG Met 205	ATG Met	ATG Met	AAC Asn	624
TGG Trp	TCG Ser 210	CCT Pro	ACA Thr	ACG Thr	GCC Ala	CTG Leu 215	GTG Val	GTA Val	TCG Ser	CAG Gln	CTG Leu 220	CTC Leu	CGG Arg	ATC Ile	CCA Pro	672

CAA Gln 225	GCT Ala	GTC Val	GTG Val	GAC Asp	ATG Met 230	GTG Val	GCG Ala	GGG Gly	GCC Ala	CAT His 235	TGG Trp	GGA Gly	GTC Val	CTG Leu	GCG Ala 240	720
GGT Gly	CTC Leu	GCC Ala	TAC Tyr	TAT Tyr 245	TCC Ser	ATG Met	GTG Val	GGG Gly	AAC Asn 250	TGG Trp	GCT Ala	AAG Lys	GTT Val	TTG Leu 255	ATT Ile	768
		CTA Leu					TAAT	AG								795
(2)	INFO	RMAT	CION	FOR	SEQ	ID N	10: 6	5:								
	(	(E		ENGTI PE:	H: 26 amir	33 am	nino cid	rics: acid								
	(ii)	MOI	LECUI	LE TY	PE:	prot	cein									
	(xi)	SEÇ	QUENC	CE DE	ESCRI	PTI	ON: S	SEQ :	ID NO	): 6:	:					
Met 1	Leu	Gly	Lys	Val 5	Ile	Asp	Thr	Leu	Thr 10	Cys	Gly	Phe	Ala	Asp 15	Leu	
TVal	Gly	Tyr	Ile 20	Pro	Leu	Val	Gly	Ala 25	Pro	Leu	Gly	Gly	Ala 30	Ala	Arg	
Eala E	Leu	Ala 35	His	Gly	Val	Arg	Val 40	Leu	Glu	Asp	Gly	Val 45	Asn	Tyr	Ala	
-Thr	Gly 50	Asn	Leu	Pro	Gly	Cys 55	Ser	Phe	Ser	Ile	Phe 60	Leu	Leu	Ala	Leu	
Leu 65	Ser	Суѕ	Leu	Thr	Val 70	Pro	Ala	Ser	Ala	Tyr 75	Glu	Val	Arg	Asn	Val 80	
Ser	Gly	Met	Tyr	His 85	Val	Thr	Asn	Asp	Cys 90	Ser	Asn	Ser	Ser	Ile 95	Val	
Tyr	Glu	Ala	Ala 100	Asp	Met	Ile	Met	His 105	Thr	Pro	Gly	Cys	Val 110	Pro	Cys	
Val	Arg	Glu 115	Asn	Asn	Ser	Ser	Arg 120	Cys	Trp	Val	Ala	Leu 125	Thr	Pro	Thr	
Leu	Ala 130	Ala	Arg	Asn	Ala	Ser 135	Val	Pro	Thr	Thr	Thr 140	Ile	Arg	Arg	His	
Val 145	Asp	Leu	Leu	Val	Gly 150	Ala	Ala	Ala	Phe	Cys 155	Ser	Ala	Met	Tyr	Val 160	
Gly	Asp	Leu	Cys	Gly 165	Ser	Val	Phe	Leu	Val 170		Gln	Leu	Phe	Thr 175	Ile	
Ser	Pro	Arg	Arg 180	His	Glu	Thr	Val	Gln 185	Asp	Cys	Asn	Cys	Ser 190	Ile	Tyr	

Pro	Gly	His 195	Ile	Thr	Gly	His	Arg 200	Met	Ala	Trp	Asp	Met 205	Met	Met	Asn	
Trp	Ser 210	Pro	Thr	Thr	Ala	Leu 215	Val	Val	Ser	Gln	Leu 220	Leu	Arg	Ile	Pro	
Gln 225	Ala	Val	Val	Asp	Met 230	Val	Ala	Gly	Ala	His 235	Trp	Gly	Val	Leu	Ala 240	
Gly	Leu	Ala	Tyr	Tyr 245	Ser	Met	Val	Gly	Asn 250	Trp	Ala	Lys	Val	Leu 255	Ile	
Val	Met	Leu	Leu 260	Phe	Ala	Pro										
(2)	INFO	RMAT	'ION	FOR	SEQ	ID N	10:	7:								
	(i)	(E		ENGTH (PE: TRANI	I: 63 nucl	33 ba Leic ESS:	ase pacionsing	pairs i	3							
	(ii)	MOI	ECUI	LE TY	PE:	CDNA	Ą									
	(iii)	HYE	POTHE	ETICA	AL: 1	10										
The state of the s	(iii)	ANT	:I-SE	ENSE:	: NO											
	(ix)		ATURE A) NA B) LO	AME/E			630									
-	(ix)		ATURE A) NA B) LO	AME/				tide								
	(xi	SE(	QUENC	CE DI	ESCR:	IPTI	: NC	SEQ :	ID NO	o: 7	:					
ATG Met 1	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACG Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
ATG Met	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala	CCC Pro	CTA Leu	GGG Gly	GGT Gly	GCT Ala 30	GCC Ala	AGA Arg	96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	Leu	GAA Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
ACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCT Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTA Leu	192
CTG Leu 65	Ser	TGT Cys	CTG Leu	ACC Thr	ATT Ile 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAG Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240

TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
					GCC Ala											432
GTC Val 145	GAT Asp	TTG Leu	CTC Leu	GTT Val	GGG Gly 150	GCG Ala	GCT Ala	GCT Ala	TTC Phe	TGT Cys 155	TCC Ser	GCT Ala	ATG Met	TAC Tyr	GTG Val 160	480
VEGG VEGLY	GAT Asp	CTC Leu	TGC Cys	GGA Gly 165	TCT Ser	GTC Val	TTC Phe	CTC Leu	GTC Val 170	TCC Ser	CAG Gln	CTG Leu	TTC Phe	ACC Thr 175	ATC Ile	528
TrcG Ser																576
LCCC Pro	GGC Gly	CAC His 195	ATA Ile	ACA Thr	GGT Gly	CAC His	CGT Arg 200	ATG Met	GCT Ala	TGG Trp	GAT Asp	ATG Met 205	ATG Met	ATG Met	AAC Asn	624
TGG	TAA:	FAG														633

#### (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 209 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu 1 5 10 15

Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 55 60

Leu 65	Ser	Cys	Leu	Thr	Ile 70	Pro	Ala	Ser	Ala	Tyr 75	Glu	Val	Arg	Asn	Val 80	
Ser	Gly	Met	Tyr	His 85	Val	Thr	Asn	Asp	Cys 90	Ser	Asn	Ser	Ser	Ile 95	Val	
Tyr	Glu	Ala	Ala 100	Asp	Met	Ile	Met	His 105	Thr	Pro	Gly	Cys	Val 110	Pro	Cys	
Val	Arg	Glu 115	Asn	Asn	Ser	Ser	Arg 120	Cys	Trp	Val	Ala	Leu 125	Thr	Pro	Thr	
Leu	Ala 130	Ala	Arg	Asn	Ala	Ser 135	Val	Pro	Thr	Thr	Thr 140	Ile	Arg	Arg	His	
Val 145	Asp	Leu	Leu	Val	Gly 150	Ala	Ala	Ala	Phe	Cys 155	Ser	Ala	Met	Tyr	Val 160	
⊑Gly II	Asp	Leu	Cys	Gly 165	Ser	Val	Phe	Leu	Val 170	Ser	Gln	Leu	Phe	Thr 175	Ile	
¶Ser	Pro	Arg	Arg 180	His	Glu	Thr	Val	Gln 185	Asp	Cys	Asn	Cys	Ser 190	Ile	Tyr	
EPro	Gly	His 195	Ile	Thr	Gly	His	Arg 200	Met	Ala	Trp	Asp	Met 205	Met	Met	Asn	
Trp																
<b>(2)</b>	INF	ORMA!	rion	FOR	SEQ	ID 1	: : OV.	9:								
2000 2000 2000 2000 2000 2000 2000 200	(i)	() () ()	A) L: B) T' C) S'	ENGT: YPE: TRAN	HARAC H: 48 nuc: DEDNI DGY:	33 ba Leic ESS:	ase pacionsino	pair: d	s							
	(ii	) MO	LECU:	LE T	YPE:	cDN	A									
	(iii	) HY	POTH:	ETIC	AL: 1	ON										
	(iii	) AN'	TI-S	ENSE	: NO											
	(ix	()		AME/	KEY:											
	(ix	(,	ATUR A) N B) L	AME/	KEY: ION:	mat	_pep 477	tide								
	(xi	) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0: 9	:					
ATG Met 1	CCC Pro	GGT Gly	TGC Cys	TCT Ser 5	TTC Phe	TCT Ser	ATC Ile	TTC Phe	CTC Leu 10	Leu	GCC Ala	CTG Leu	CTG Leu	TCC Ser 15	TGT Cys	48
CTG	ACC	ATA	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	96

Leu	Thr	Ile	Pro 20	Ala	Ser	Ala	Tyr	Glu 25	Val	Arg	Asn	Val	Ser 30	Gly	Val	
TAC Tyr	CAT His	GTC Val 35	ACG Thr	AAC Asn	GAC Asp	TGC Cys	TCC Ser 40	AAC Asn	TCA Ser	AGC Ser	ATA Ile	GTG Val 45	TAT Tyr	GAG Glu	GCA Ala	144
GCG Ala	GAC Asp 50	ATG Met	ATC Ile	ATG Met	CAC His	ACC Thr 55	CCC Pro	GGG Gly	TGC Cys	GTG Val	CCC Pro 60	TGC Cys	GTT Val	CGG Arg	GAG Glu	192
GGC Gly 65	AAC Asn	TCC Ser	TCC Ser	CGT Arg	TGC Cys 70	TGG Trp	GTG Val	GCG Ala	CTC Leu	ACT Thr 75	CCC Pro	ACG Thr	CTC Leu	GCG Ala	GCC Ala 80	240
AGG Arg	AAC Asn	GCC Ala	AGC Ser	GTC Val 85	CCC Pro	ACA Thr	ACG Thr	ACA Thr	ATA Ile 90	CGA Arg	CGC Arg	CAC His	GTC Val	GAT Asp 95	TTG Leu	288
ECTC Leu																336
TGC Cys																384
CGG Arg	CAT His 130	CAA Gln	ACA Thr	GTA Val	CAG Gln	GAC Asp 135	TGC Cys	AAC Asn	TGC Cys	TCA Ser	ATC Ile 140	TAT Tyr	CCC	GGC Gly	CAT His	432
GTA Val L145															TAATAG 160	483
(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO:	10:								
		(i) :	SEQUI	ENCE	CHA	RACT	ERIS	rics	:							

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys 1 5 10 15

Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val 20 25 30

Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala 35 40 45

Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu 50 55 60

Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala 65 70 75 80

Arg	Asn	Ala	Ser	Val 85	Pro	Thr	Thr	Thr	Ile 90	Arg	Arg	His	Val	Asp 95	Leu		
Leu	Val	Gly	Ala 100	Ala	Ala	Phe	Cys	Ser 105	Ala	Met	Tyr	Val	Gly 110	Asp	Leu		
Cys	Gly	Ser 115	Val	Phe	Leu	Val	Ser 120	Gln	Leu	Phe	Thr	Phe 125	Ser	Pro	Arg		
Arg	His 130	Gln	Thr	Val	Gln	Asp 135	Cys	Asn	Cys	Ser	Ile 140	Tyr	Pro	Gly	His		
Val 145	Ser	Gly	His	Arg	Met 150	Ala	Trp	Asp	Met	Met 155	Met	Asn	Trp	Ser			
(2)				FOR													
	(i)	() ()	A) LI B) T: C) S'	CE CH ENGTH YPE: TRANI DPOLO	H: 48 nucl	30 ba Leic ESS:	ase p acid	pairs i	3								
	(ii	MO	LECU	LE T	PE:	CDNA	F.										
	(iii)	HY!	POTH	ETICA	AL: 1	NO											
	(iii	) AN'	ri-si	ENSE	: NO												
T.	(ix)	•	A) N	E: AME/I OCATI			477										
	(ix		A) N	E: AME/! OCAT!				tide									
,	(xi	) SE	QUEN	CE DI	ESCR	IPTI	ON:	SEQ	ID N	0: 1	1:						
ATG Met 1	TCC Ser	GGT Gly	TGC Cys	TCT Ser 5	TTC Phe	TCT Ser	ATC Ile	TTC Phe	CTC Leu 10	TTG Leu	GCC Ala	CTG Leu	CTG Leu	TCC Ser 15	TGT Cys	48	
CTG Leu	ACC Thr	ATA Ile	CCA Pro 20	GCT Ala	TCC Ser	GCT Ala	TAT Tyr	GAA Glu 25	GTG Val	CGC Arg	AAC Asn	GTG Val	TCC Ser 30	GGG Gly	GTG Val	96	
TAC Tyr	CAT His	GTC Val 35	ACG Thr	AAC Asn	GAC Asp	TGC Cys	TCC Ser 40	AAC Asn	TCA Ser	AGC Ser	ATA Ile	GTG Val 45	TAT	GAG Glu	GCA Ala	144	
GCG Ala	GAC Asp 50	Met	ATC Ile	ATG Met	CAC His	ACC Thr 55	CCC Pro	GGG Gly	TGC Cys	GTG Val	CCC Pro 60	TGC Cys	GTT Val	CGG Arg	GAG Glu	192	
GGC Gly 65	Asn	TCC Ser	TCC Ser	CGT Arg	TGC Cys 70	Trp	GTG Val	GCG Ala	CTC Leu	ACT Thr 75	Pro	ACG Thr	CTC Leu	GCG Ala	GCC Ala 80	240	j

AGG Arg	AAC Asn	GCC Ala	AGC Ser	GTC Val 85	CCC Pro	ACA Thr	ACG Thr	ACA Thr	ATA Ile 90	CGA Arg	CGC Arg	CAC His	GTC Val	GAT Asp 95	TTG Leu	288	}
CTC Leu	GTT Val	GGG Gly	GCT Ala 100	GCT Ala	GCT Ala	TTC Phe	TGT Cys	TCC Ser 105	GCT Ala	ATG Met	TAC Tyr	GTG Val	GGG Gly 110	GAT Asp	CTC Leu	336	ŝ
TGC Cys	GGA Gly	TCT Ser 115	GTT Val	TTC Phe	CTT Leu	GTT Val	TCC Ser 120	CAG Gln	CTG Leu	TTC Phe	ACC Thr	TTC Phe 125	TCA Ser	CCT Pro	CGC Arg	384	ł
CGG Arg	CAT His 130	CAA Gln	ACA Thr	GTA Val	CAG Gln	GAC Asp 135	TGC Cys	AAC Asn	TGC Cys	TCA Ser	ATC Ile 140	TAT Tyr	CCC Pro	GGC Gly	CAT His	432	2
145	TCA Ser	GGT Gly	CAC His	CGC Arg	ATG Met 150	GCT Ala	TGG Trp	GAT Asp	ATG Met	ATG Met 155	ATG Met	AAC Asn	TGG Trp	TAAT	AG	480	)
⊈ ⊈(2)	INFO	ORMAT	TION	FOR	SEQ	ID S	10: 3	12:									
	1	( <i>I</i>	A) LE B) Ti	ENGTI YPE:		68 an	nino cid	TICS:									
	(ii)	MOI	LECUI	LE T	YPE:	prot	cein										
<b>:</b>																	
STATE OF THE PARTY	(xi)	SE	QUEN	CE DI	ESCRI	[PTI	ЭИ: 3	SEQ :	ED NO	): 12	2:						
I I E Met 1												Leu	Leu	Ser 15	Cys		
I Met 1	Ser	Gly	Cys	Ser 5	Phe	Ser	Ile		Leu 10	Leu	Ala						
Met 1 Leu	Ser Thr	Gly	Cys Pro 20	Ser 5 Ala	Phe	Ser	Ile	Phe	Leu 10 Val	Leu	Ala Asn	Val	Ser 30	Gly	Val		
Met 1 Leu Tyr	Ser Thr His	Gly Ile Val 35	Cys Pro 20 Thr	Ser 5 Ala Asn	Phe Ser Asp	Ser Ala Cys	Ile Tyr Ser 40	Phe Glu 25	Leu 10 Val Ser	Leu Arg Ser	Ala Asn Ile	Val Val 45	Ser 30 Tyr	Gly Glu	Val Ala		
Met 1 Leu Tyr	Ser Thr His	Gly Ile Val 35	Cys Pro 20 Thr	Ser 5 Ala Asn Met	Phe Ser Asp	Ser Ala Cys Thr	Ile Tyr Ser 40	Phe Glu 25 Asn	Leu 10 Val Ser	Leu Arg Ser Val	Ala Asn Ile Pro 60	Val Val 45 Cys	Ser 30 Tyr	Gly Glu Arg	Val Ala Glu		
Met 1 Leu Tyr Ala Gly 65	Ser Thr His Asp 50 Asn	Gly Ile Val 35 Met Ser	Pro 20 Thr Ile Ser	Ser 5 Ala Asn Met Arg	Phe Ser Asp His Cys 70	Ser Ala Cys Thr 55	Tyr Ser 40 Pro	Phe Glu 25 Asn Gly	Leu 10 Val Ser Cys Leu	Leu Arg Ser Val Thr 75	Ala Asn Ile Pro 60 Pro	Val Val 45 Cys Thr	Ser 30 Tyr Val Leu	Gly Glu Arg Ala	Val Ala Glu Ala 80		
Met 1 Leu Tyr Ala Gly 65 Arg	Ser Thr His Asp 50 Asn	Gly Ile Val 35 Met Ser Ala	Pro 20 Thr Ile Ser	Ser 5 Ala Asn Met Arg Val 85	Phe Ser Asp His Cys 70 Pro	Ser Ala Cys Thr 55 Trp	Tyr Ser 40 Pro Val	Glu 25 Asn Gly Ala	Leu 10 Val Ser Cys Leu Ile 90	Leu Arg Ser Val Thr 75	Ala Asn Ile Pro 60 Pro Arg	Val Val 45 Cys Thr	Ser 30 Tyr Val Leu Val	Gly Glu Arg Ala Asp 95	Val Ala Glu Ala 80 Leu		
Met 1 Leu Tyr Ala Gly 65 Arg Leu	Ser Thr His Asp 50 Asn Val	Gly Ile Val 35 Met Ser Ala Gly	Pro 20 Thr Ile Ser Ser Ala 100	Ser 5 Ala Asn Met Arg Val 85 Ala	Phe Ser Asp His Cys 70 Pro	Ser Ala Cys Thr 55 Trp Thr	Tyr Ser 40 Pro Val Thr	Glu 25 Asn Gly Ala Thr Ser 105 Gln	Leu 10 Val Ser Cys Leu Ile 90 Ala	Leu Arg Ser Val Thr 75 Arg	Ala Asn Ile Pro 60 Pro Arg	Val Val 45 Cys Thr His	Ser 30 Tyr Val Leu Val Gly 110	Gly Glu Arg Ala Asp 95 Asp	Val Ala Glu Ala 80 Leu Leu		
Met 1 Leu Tyr Ala Gly 65 Arg Leu Cys	Thr His Asp 50 Asn Val	Gly Ile Val 35 Met Ser Ala Gly Ser 115 Gln	Pro 20 Thr Ile Ser Ser Ala 100 Val	Ser 5 Ala Asn Met Arg Val 85 Ala Phe	Phe Ser Asp His Cys 70 Pro Ala Leu	Ser Ala Cys Thr 55 Trp Thr Phe Val	Ile Tyr Ser 40 Pro Val Thr Cys Ser 120 Cys	Glu 25 Asn Gly Ala Thr Ser 105 Gln	Leu 10 Val Ser Cys Leu Ile 90 Ala	Leu Arg Ser Val Thr 75 Arg Met	Ala Asn Ile Pro 60 Pro Arg Tyr	Val 45 Cys Thr His Val Phe 125	Ser 30 Tyr Val Leu Val Gly 110 Ser	Gly Glu Arg Ala Asp 95 Asp	Val Ala Glu Ala 80 Leu Leu Arg		

(	2)	INFO	RMAT	ION	FOR	SEQ	ID N	0: 1	3:								
		(i)	(A (B (C	) LE ) TY () ST	E CH INGTH IPE: IRAND IPOLO	: 63 nucl EDNE	6 ba eic SS:	se p acid sing	airs								
		(ii)	MOL	ECUL	E TY	PE:	CDNA										
	(	iii)	HYP	OTHE	TICA	L: N	10										
	(	iii)	ANT	'I-SE	ENSE:	NO											
		(ix)		A) NA	E: AME/F CATI			33									
		(ix)	( P	A) NA	E: AME/F DCATI	KEY:	mat_ 16	pept 30	ide								
3 : :		(xi)	SEC	QUENC	CE DE	ESCRI	PTIC	N: S	SEQ I	D NC	): 13	3:					
EA ►M	TG let 1	CTG Leu	GGT Gly	AAG Lys	GCC Ala 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACG Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
	TG al	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
G A	CC la	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAA Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
A	CA.	GGG Gly 50	AAT Asn	TTG Leu	CCT Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTA Leu	192
I	CTG Leu 65	TCC Ser	TGT Cys	CTA Leu	ACC Thr	ATT Ile 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAC Tyr 75	GAG Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240
ï	CC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
1	TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
7	GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
																~~~	430

CTC GCG GCT AGG AAC GCC AGC ATC CCC ACT ACA ACA ATA CGA CGC CAC

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	Leu	Ala 130	Ala	Arg	Asn	Ala	Ser 135	Ile	Pro	Thr	Thr	Thr 140	Ile	Arg	Arg	His	
		GAT Asp															480
	GGG Gly	GAT Asp	CTC Leu	TGC Cys	GGA Gly 165	TCT Ser	GTC Val	TTC Phe	CTC Leu	GTC Val 170	TCC Ser	CAG Gln	CTG Leu	TTC Phe	ACC Thr 175	ATC Ile	528
		CCT Pro															576
		GGC Gly															624
		TAC Tyr 210	TAA	ΓAG													640
	(2)	INFO	ORMA:	rion	FOR	SEQ	ID N	NO: 3	L4:								
			-	A) L	ENGT	H: 23		nino									
				) T(													
,		(ii)		) T(	OPOLO	OGY:	line	ear									
			1)	D) TO	DPOLO	OGY: YPE:	prot	ear cein	SEQ I	ID NO	D: 1	4:					
	Met 1		(I ) MOI ) SE(	D) TO LECUI QUENO	DPOLO	OGY: YPE: ESCR:	line prot	ear cein ON: S					Phe	Ala	Asp 15	Leu	
æi æi:	1	(xi)	(I ) MOI ) SE( Gly	D) TO LECUI QUENO Lys	DPOLO LE TY CE DE Ala 5	OGY: YPE: ESCRI	line prot IPTIC Asp	ear cein ON: S	Leu	Thr 10	Cys	Gly			15		
æi æi:	l Val	(xi)	(I) MOD SEC	D) TO LECUI QUENO Lys Ile 20	DPOLO LE TY CE DE Ala 5	DGY: YPE: ESCR: Ile Leu	line prot PTIC Asp	ear cein ON: S Thr	Leu Ala 25	Thr 10 Pro	Cys Leu	Gly	Gly	Ala 30	15 Ala	Arg	
æi æi:	Val Ala	(xi) Leu Gly	(I ) MOI ) SE( Gly Tyr Ala 35	LECUI QUENC Lys Ile 20	DPOLO LE TY CE DE Ala 5 Pro Gly	OGY: YPE: ESCRI	line prot PTIC Asp Val Arg	ear cein ON: S Thr Gly Val 40	Leu Ala 25 Leu	Thr 10 Pro	Cys Leu Asp	Gly Gly Gly	Gly Val 45	Ala 30 Asn	15 Ala Tyr	Arg Ala	
æi æi:	Val Ala Thr	(xi) Leu Gly Leu	MOD SEQ Gly Tyr Ala 35 Asn	LECUI QUENC Lys Ile 20 His	DPOLO DPOLO DE TY Ala 5 Pro Gly Pro	OGY: YPE: YPE: Leu Val Gly	line prot PTIC Asp Val Arg Cys 55	tein ON: S Thr Gly Val 40 Ser	Leu Ala 25 Leu Phe	Thr 10 Pro Glu Ser	Cys Leu Asp	Gly Gly Phe 60	Gly Val 45 Leu	Ala 30 Asn Leu	15 Ala Tyr Ala	Arg Ala Leu	
æi æi:	Val Ala Thr Leu 65	(xi) Leu Gly Leu Gly 50	(I ) MOD ) SEQ Gly Tyr Ala 35 Asn Cys	LECUI QUENC Lys Ile 20 His Leu	DPOLO DPOLO DPOLO DPOLO Ala 5 Pro Gly Pro Thr	OGY: YPE: YPE: Leu Val Gly Ile 70	line prot PTIC Asp Val Arg Cys 55	tein ON: S Thr Gly Val 40 Ser Ala	Leu Ala 25 Leu Phe	Thr 10 Pro Glu Ser	Cys Leu Asp Ile Tyr 75	Gly Gly Phe 60	Gly Val 45 Leu Val	Ala 30 Asn Leu Arg	15 Ala Tyr Ala Asn	Arg Ala Leu Val 80	
æi æi:	Val Ala Thr Leu 65 Ser	(xi) Leu Gly Leu Gly 50 Ser	MOD SEG Gly Tyr Ala 35 Asn Cys	LECUI QUENC Lys Ile 20 His Leu Leu	DPOLO DPOLO DPOLO DPOLO DPOLO Ala 5 Pro Gly Pro Thr His 85	OGY: YPE: YPE: Leu Val Gly Ile 70 Val	line prot PTIC Asp Val Arg Cys 55 Pro Thr	tein ON: S Thr Gly Val 40 Ser Ala Asn	Leu Ala 25 Leu Phe Ser Asp	Thr 10 Pro Glu Ser Ala Cys 90	Cys Leu Asp Ile Tyr 75 Ser	Gly Gly Phe 60 Glu Asn	Gly Val 45 Leu Val	Ala 30 Asn Leu Arg	15 Ala Tyr Ala Asn Ile 95	Arg Ala Leu Val 80 Val	
æi æi:	Val Ala Thr Leu 65 Ser	(xi) Leu Gly Leu Gly 50 Ser	MOD SEG Gly Tyr Ala 35 Asn Cys Met	LECUI QUENC Lys Ile 20 His Leu Leu Tyr	DPOLO DPOLO DPOLO DPOLO DPOLO DPOLO Ala 5 Pro Gly Pro Thr His 85 Asp	OGY: YPE: YPE: Leu Val Gly Ile 70 Val Met	line prot PTIC Asp Val Arg Cys 55 Pro Thr	tein ON: S Thr Gly Val 40 Ser Ala Asn Met	Leu Ala 25 Leu Phe Ser Asp His 105	Thr 10 Pro Glu Ser Ala Cys 90 Thr	Cys Leu Asp Ile Tyr 75 Ser Pro	Gly Gly Phe 60 Glu Asn	Gly Val 45 Leu Val Ser Cys	Ala 30 Asn Leu Arg Ser Val 110	15 Ala Tyr Ala Asn Ile 95 Pro	Arg Ala Leu Val 80 Val Cys	

		130					135					140					
	Val 145	Asp	Leu	Leu	Val	Gly 150	Ala	Ala	Ala	Phe	Cys 155	Ser	Ala	Met	Tyr	Val 160	
	Gly	Asp	Leu	Cys	Gly 165	Ser	Val	Phe	Leu	Val 170	Ser	Gln	Leu	Phe	Thr 175	Ile	
	Ser	Pro	Arg	Arg 180	His	Glu	Thr	Val	Gln 185	Asp	Cys	Asn	Cys	Ser 190	Ile	Tyr	
	Pro	Gly	His 195	Ile	Thr	Gly	His	Arg 200	Met	Ala	Trp	Asp	Met 205	Met	Met	Asn	
	Trp	Tyr 210															
-	(2)	INFO	DRMAT	TION	FOR	SEQ	ID 1	NO: :	15:								
			SE( () ()	QUENCA) LIB) T'C) S'	CE CI ENGTI YPE: IRANI	HARACH: 26 nucl	CTER 6 bas Leic ESS:	ISTIC se pa acic sinc	CS: airs								
Ξ		(ii)	MOI	LECUI	LE T	YPE:	cDN	Ą									
-		(iii)	HYI	POTH	ETICA	AL: 1	NO										
-		(iii)	AN:	ri-Si	ENSE	: NO											
		(xi)	SE	QUEN	CE DI	ESCR	IPTI	ON:	SEQ :	ID NO	D: 15	5:					
	ATG	CCCG	GTT (	GCTC'	rttc:	rc TA	ATCT'	Γ									26
	(2)	INFO	ORMA:	rion	FOR	SEQ	ID I	NO:	16:								
		(i)	( ) ( )	A) L: B) T' C) S'	ENGTI YPE: IRANI	HARAG H: 26 nucl DEDNI DGY:	6 ba: leic ESS:	se pacionsino	airs d								
		(ii)	) MOI	LECU:	LE T	YPE:	CDN	Ą									
		(iii)	HY)	POTH	ETIC	AL: 1	ON										
		(iii)	AN'	ri-si	ENSE	: NO											
		(xi)	) SE	QUEN	CE DI	ESCR:	IPTI(	: NC	SEQ :	ID N	D: 1	6:					
	ATG	TTGG	GTA A	AGGT	CATC	GA T	ACCC'	ľ									26
	(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	NO:	17:								
		(i)	SE	OUEN	CE C	HARA	CTER	ISTI	CS:								

		<ul><li>(A) LENGTH: 30 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
	(ii)	MOLECULE TYPE: cDNA	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: YES	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 17:	
CTA	TTAGG	AC CAGTTCATCA TCATATCCCA	30
<u>_</u> (2)	INFO	RMATION FOR SEQ ID NO: 18:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 27 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
Marie Control	(ii)	MOLECULE TYPE: cDNA	
	(iii)	HYPOTHETICAL: NO	
Flames	(iii)	ANTI-SENSE: YES	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 18:	
-	ATTACC.	AG TTCATCATCA TATCCCA	27
(2)	INFO	RMATION FOR SEQ ID NO: 19:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 36 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
		SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
ATA	ACGACG	CC ACGTCGATTC CCAGCTGTTC ACCATC	36
(2)	INFO	RMATION FOR SEQ ID NO: 20:	

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs

		(0	C) SI	PE: RAND POLC	EDNE	SS:	sing									
	(ii)	MOL	ECUL	E TY	PE:	CDNA										
(	iii)	HYE	POTHE	TICA	AL: N	10										
(	iii)	ANT	I-SE	NSE:	YES	;										
	(xi)	SEÇ	QUENC	CE DE	SCRI	PTIC	N: S	SEQ I	D NC	): 20	:					
GATG	GTGA	AC A	AGCTO	GGAA	AT CO	ACGI	'GGCG	TCG	TAT							36
• •	INFO	RMAI	CION	FOR	SEQ	ID N	10: 2	21:								
	(i)	( <i>P</i> (E	A) LE 3) TY C) ST	E CHENGTH PE: RAND	H: 72 nucl DEDNE	23 ba .eic :SS:	se p acid sing	oairs i	3							
	(ii)	MOI	LECUI	LE TY	YPE:	CDNA	7									
3	iii)	HYE	POTHE	ETICA	AL: N	10										
	iii)	ANT	ri-se	ENSE:	NO.											
	(ix)	(P	A) NA	E: AME/F DCATI			720									
	(ix)	(P	ATURE A) NA B) LO	E: AME/F DCATI	KEY:	mat 1	_pept 717	ide								
	(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	on: s	SEQ :	D NO	): 2	L:					
	TTG Leu															48
GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
ACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192
CTG Leu 65	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240

	TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
	Tyr	Glu	Ala	Ala 100	Asp	Met	ATC Ile	Met	His 105	Thr	Pro	Gly	Cys	Val 110	Pro	Cys	336
	GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
	CTC Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
	GTC Val 145	GAT Asp	TCC Ser	CAG Gln	CTG Leu	TTC Phe 150	ACC Thr	ATC Ile	TCG Ser	CCT Pro	CGC Arg 155	CGG Arg	CAT His	GAG Glu	ACG Thr	GTG Val 160	480
I	CAG Gln	GAC Asp	TGC Cys	AAT Asn	TGC Cys 165	TCA Ser	ATC Ile	TAT Tyr	CCC Pro	GGC Gly 170	CAC His	ATA Ile	ACG Thr	GGT Gly	CAC His 175	CGT Arg	528
	ATG Met	GCT Ala	TGG Trp	GAT Asp 180	ATG Met	ATG Met	ATG Met	AAC Asn	TGG Trp 185	TCG Ser	CCT Pro	ACA Thr	ACG Thr	GCC Ala 190	CTG Leu	GTG Val	576
	Val	Ser	Gln 195	Leu	Leu	Arg	ATC Ile	Pro 200	Gln	Ala	Val	Val	Asp 205	Met	Val	Ala	624
	GGG Gly	GCC Ala 210	CAT His	TGG Trp	GGA Gly	GTC Val	CTG Leu 215	GCG Ala	GGT Gly	CTC Leu	GCC Ala	TAC Tyr 220	TAT Tyr	TCC Ser	ATG Met	GTG Val	672
	GGG Gly 225	AAC Asn	TGG Trp	GCT Ala	AAG Lys	GTT Val 230	TTG Leu	ATT Ile	GTG Val	ATG Met	CTA Leu 235	CTC Leu	TTT Phe	GCT Ala	CCC	TAATAG 240	723

## (2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 239 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$ 

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 55 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 105 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Wal Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val **1145** Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg 170 Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val 180 z Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val 210 Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro 230 <u>1</u> 225

- (2) INFORMATION FOR SEQ ID NO: 23:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 561 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
    - (ix) FEATURE:
      - (A) NAME/KEY: CDS
      - (B) LOCATION: 1..558
    - (ix) FEATURE:
      - (A) NAME/KEY: mat\_peptide
      - (B) LOCATION: 1..555
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

A: Me	rG ( et )	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACA Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
G: Va	rg (	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
G( A)	CC ( la :	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
A) Tl	CA (	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192
I.	eu	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240
TO SOLUTION OF THE SECOND SECO	CC er	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
LT	AT yr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
L v	TT :	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
E C	eu .	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
V	TC al 45	GAT Asp	TCC Ser	CAG Gln	CTG Leu	TTC Phe 150	ACC Thr	ATC Ile	TCG Ser	CCT Pro	CGC Arg 155	CGG Arg	CAT His	GAG Glu	ACG Thr	GTG Val 160	480
C. G	ĀG ln	GAC Asp	TGC Cys	AAT Asn	TGC Cys 165	TCA Ser	ATC Ile	TAT Tyr	CCC Pro	GGC Gly 170	CAC His	ATA Ile	ACG Thr	GGT Gly	CAC His 175	CGT Arg	528
					ATG Met					TAA	TAG						561

## (2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 185 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 20 25 30

10

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val 85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110

TVal Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His
130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg 165 170 175

Met Ala Trp Asp Met Met Met Asn Trp
180 185

#### (2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 606 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..603
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 1..600
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

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ATG Met 1	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACA Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
ACA Thr	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192
□Leu □ 65	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240
TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
TAT LTyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC	TGC Cys	336
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
∏ ECTC LLeu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
GTC Val 145	Asp	TCC Ser	CAG Gln	CTG Leu	TTC Phe 150	Thr	ATC Ile	TCG Ser	CCT Pro	CGC Arg 155	CGG Arg	CAT His	GAG Glu	ACG Thr	GTG Val 160	480
CAG	GAC	TGC Cys	AAT Asn	TGC Cys 165	TCA	ATC	TAT Tyr	Pro	Gly	His	Ile	Thr	Gly	His	CGT Arg	528
ATG Met	GCT Ala	TGG Trp	GAT Asp 180	Met	ATG Met	ATG Met	AAC Asn	TGG Trp 185	Ser	CCT Pro	ACA Thr	ACG Thr	GCC Ala 190	Leu	GTG Val	576
			Leu			ATC Ile			TAG							606

## (2) INFORMATION FOR SEQ ID NO: 26:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 200 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu 1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val 145 150 150 155

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg

Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val 180 185 190

Val Ser Gln Leu Leu Arg Ile Leu 195 200

#### (2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 636 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide (B) LOCATION: 1..630

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

	,,		-													
ATG Met 1	TTG Leu	GGT Gly	AAG Lys	GTC Val 5	ATC Ile	GAT Asp	ACC Thr	CTT Leu	ACA Thr 10	TGC Cys	GGC Gly	TTC Phe	GCC Ala	GAC Asp 15	CTC Leu	48
GTG Val	GGG Gly	TAC Tyr	ATT Ile 20	CCG Pro	CTC Leu	GTC Val	GGC Gly	GCC Ala 25	CCC Pro	CTA Leu	GGG Gly	GGC Gly	GCT Ala 30	GCC Ala	AGG Arg	96
GCC Ala	CTG Leu	GCG Ala 35	CAT His	GGC Gly	GTC Val	CGG Arg	GTT Val 40	CTG Leu	GAG Glu	GAC Asp	GGC Gly	GTG Val 45	AAC Asn	TAT Tyr	GCA Ala	144
IIACA IIThr	GGG Gly 50	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys 55	TCT Ser	TTC Phe	TCT Ser	ATC Ile	TTC Phe 60	CTC Leu	TTG Leu	GCT Ala	TTG Leu	192
CTG Leu 4 65	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val 70	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr 75	GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val 80	240
TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His 85	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys 90	TCC Ser	AAC Asn	TCA Ser	AGC Ser	ATT Ile 95	GTG Val	288
TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384
CTC Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432
GTC Val 145	GAT Asp	TCC Ser	CAG Gln	CTG Leu	TTC Phe 150	ACC Thr	ATC Ile	TCG Ser	CCT Pro	CGC Arg 155	CGG Arg	CAT His	GAG Glu	ACG Thr	GTG Val 160	480
CAG Gln	GAC Asp	TGC Cys	AAT Asn	TGC Cys 165	TCA Ser	ATC Ile	TAT Tyr	CCC Pro	GGC Gly 170	CAC His	ATA Ile	ACG Thr	GGT Gly	CAC His 175	CGT Arg	528
ATG Met	GCT Ala	TGG Trp	GAT Asp 180	Met	ATG Met	ATG Met	AAC Asn	TGG Trp 185	TCG Ser	CCT Pro	ACA Thr	ACG Thr	GCC Ala 190	Leu	GTG Val	576
GTA Val	TCG Ser	CAG Gln 195	CTG Leu	CTC Leu	CGG Arg	ATC Ile	GTG Val 200	ATC Ile	GAG Glu	GGC Gly	AGA Arg	CAC His 205	His	CAC His	CAC His	624
	CAC His		TAG													636

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## (2) INFORMATION FOR SEQ ID NO: 28:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 210 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu ₹al Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu \*\*Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val 85 90 95 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 105 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val 180 Val Ser Gln Leu Leu Arg Ile Val Ile Glu Gly Arg His His His 200 His His

(2) INFORMATION FOR SEQ ID NO: 29:

210

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 630 base pairs

(	(iii)	ANT	I-SE	NSE:	ИО											
	(ix)	( A	TURE () NA () LC	ME/K			i27									
	(ix)	(A	ATURE A) NA B) LC	ME/K				ide								
	(xi)	SEC	QUENC	E DE	SCRI	PTIC	N: S	EQ I	D NO	): 29	):					
ATG Met 1	GGT Gly	AAG Lys	GTC Val	ATC Ile 5	GAT Asp	ACC Thr	CTT Leu	ACG Thr	TGC Cys 10	GGA Gly	TTC Phe	GCC Ala	GAT Asp	CTC Leu 15	ATG Met	48
GGG Gly	TAC Tyr	ATC Ile	CCG Pro 20	CTC Leu	GTC Val	GGC Gly	GCT Ala	CCC Pro 25	GTA Val	GGA Gly	GGC Gly	GTC Val	GCA Ala 30	AGA Arg	GCC Ala	96
CTT Leu	GCG Ala	CAT His 35	GGC Gly	GTG Val	AGG Arg	GCC Ala	CTT Leu 40	GAA Glu	GAC Asp	GGG Gly	ATA Ile	AAT Asn 45	TTC Phe	GCA Ala	ACA Thr	144
GGG Gly	AAT Asn 50	TTG Leu	CCC Pro	GGT Gly	TGC Cys	TCC Ser 55	TTT Phe	TCT Ser	ATT Ile	TTC Phe	CTT Leu 60	CTC Leu	GCT Ala	CTG Leu	TTC Phe	192
TCT Ser 65	TGC Cys	TTA Leu	ATT Ile	CAT His	CCA Pro 70	GCA Ala	GCT Ala	AGT Ser	CTA Leu	GAG Glu 75	TGG Trp	CGG Arg	AAT Asn	ACG Thr	TCT Ser 80	240
GGC Gly	CTC Leu	TAT Tyr	GTC Val	CTT Leu 85	ACC Thr	AAC Asn	GAC Asp	TGT Cys	TCC Ser 90	AAT Asn	AGC Ser	AGT Ser	ATT Ile	GTG Val 95	TAC Tyr	288
GAG Glu	GCC Ala	GAT Asp	GAC Asp 100	GTT Val	ATT Ile	CTG Leu	CAC His	ACA Thr 105	CCC Pro	GGC Gly	TGC Cys	ATA Ile	CCT Pro 110	TGT Cys	GTC Val	336
CAG Gln	GAC Asp	GGC Gly 115	AAT Asn	ACA Thr	TCC Ser	ACG Thr	TGC Cys 120	TGG Trp	ACC Thr	CCA Pro	GTG Val	ACA Thr 125	CCT Pro	ACA Thr	GTG Val	384
GCA Ala	GTC Val 130	AAG Lys	TAC Tyr	GTC Val	GGA Gly	GCA Ala 135	ACC Thr	ACC Thr	GCT Ala	TCG Ser	ATA Ile 140	CGC Arg	AGT Ser	CAT His	GTG Val	432
GAC Asp 145	CTA Leu	TTA Leu	GTG Val	GGC Gly	GCG Ala 150	GCC Ala	ACG Thr	ATG Met	TGC Cys	TCT Ser 155	GCG Ala	CTC Leu	TAC Tyr	GTG Val	GGT Gly 160	480

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

	GAC Asp	ATG Met	TGT Cys	GGG Gly	GCT Ala 165	GTC Val	TTC Phe	CTC Leu	GTG Val	GGA Gly 170	CAA Gln	GCC Ala	TTC Phe	ACG Thr	TTC Phe 175	AGA Arg	528
	CCT Pro	CGT Arg	CGC Arg	CAT His 180	CAA Gln	ACG Thr	GTC Val	CAG Gln	ACC Thr 185	TGT Cys	AAC Asn	TGC Cys	TCG Ser	CTG Leu 190	TAC Tyr	CCA Pro	576
	GGC Gly	CAT His	CTT Leu 195	TCA Ser	GGA Gly	CAT His	CGA Arg	ATG Met 200	GCT Ala	TGG Trp	GAT Asp	ATG Met	ATG Met 205	ATG Met	AAC Asn	TGG Trp	624
	TAAT	'AG															634
			(i) S ( <i>I</i> (E	FION SEQUE A) LE B) TY	ENCE ENGTH (PE:	CHAE H: 20 ami:	RACTE 18 am	ERIST mino cid	rics	: ds							
				LECUI						- D 170	. 2/	2					
15										ID NO Cys			Ala	Asp	Leu	Met	
	1	_			5					10					15		
700	GIA	Tyr	Ile	Pro 20	Leu	Val	GIĀ	Ala	25	Val	GTĀ	GTĀ	Vai	30	Arg	ALG	
	Leu	Ala	His 35	Gly	Val	Arg	Ala	Leu 40	Glu	Asp	Gly	Ile	Asn 45	Phe	Ala	Thr	
	Gly	Asn 50		Pro	Gly	Cys	Ser 55	Phe	Ser	Ile	Phe	Leu 60	Leu	Ala	Leu	Phe	
	Ser 65	Cys	Leu	Ile	His	Pro 70	Ala	Ala	Ser	Leu	Glu 75	Trp	Arg	Asn	Thr	Ser 80	
	Gly	Leu	Tyr	Val	Leu 85	Thr	Asn	Asp	Cys	Ser 90	Asn	Ser	Ser	Ile	Val 95	Tyr	
	Glu	Ala	Asp	Asp 100	Val	Ile	Leu	His	Thr 105	Pro	Gly	Cys	Ile	Pro 110	Cys	Val	
	Gln	Asp	Gly 115		Thr	Ser	Thr	Cys 120		Thr	Pro	Val	Thr 125	Pro	Thr	Val	
	Ala	Val 130		Tyr	Val	Gly	Ala 135		Thr	Ala	Ser	Ile 140	Arg	Ser	His	Val	
	Asp 145		Leu	Val	Gly	Ala 150		Thr	Met	Cys	Ser 155	Ala	Leu	Tyr	Val	Gly 160	
	Asp	Met	Cys	Gly	Ala 165		Phe	Leu	. Val	. Gly 170	Gln	Ala	Phe	Thr	Phe 175	Arg	

?ro	Arg	Arg	His 180	Gln	Thr	Val	Gln	Thr 185	Cys	Asn	Cys	Ser	Leu 190	Tyr	Pro
Gly	His	Leu 195	Ser	Gly	His	Arg	Met 200	Ala	Trp	Asp	Met	Met 205	Met	Asn	Trp
(2)	INF	ORMA:	rion	FOR	SEQ	ID 1	NO:	31:							
	(i)	) SE(	QUEN	CE CI	HARA	CTER	ISTI	CS:							

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- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..627
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LCCATION: 1..624
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG Met 1	GGT Gly	AAG Lys	GTC Val	ATC Ile 5	GAT Asp	ACC Thr	CTA Leu	ACG Thr	TGC Cys 10	GGA Gly	TTC Phe	GCC Ala	GAT Asp	CTC Leu 15	ATG Met	4	48
GGG Gľy	TAT Tyr	ATC Ile	CCG Pro 20	CTC Leu	GTA Val	GGC Gly	GGC Gly	CCC Pro 25	ATT Ile	GGG Gly	GGC Gly	GTC Val	GCA Ala 30	AGG Arg	GCT Ala	Ġ	96
CTC Leu	GCA Ala	CAC His 35	GGT Gly	GTG Val	AGG Arg	GTC Val	CTT Leu 40	GAG Glu	GAC Asp	GGG Gly	GTA Val	AAC Asn 45	TAT Tyr	GCA Ala	ACA Thr	1	44
GGG Gly	AAT Asn 50	TTA Leu	CCC Pro	GGT Gly	TGC Cys	TCT Ser 55	TTC Phe	TCT Ser	ATC Ile	TTT Phe	ATT Ile 60	CTT Leu	GCT Ala	CTT Leu	CTC Leu	1	92
TCG Ser 65	TGT Cys	CTG Leu	ACC Thr	GTT Val	CCG Pro 70	GCC Ala	TCT Ser	GCA Ala	GTT Val	CCC Pro 75	TAC Tyr	CGA Arg	AAT Asn	GCC Ala	TCT Ser 80	2	40
GGG 31y	ATT Ile	TAT Tyr	CAT His	GTT Val 85	ACC Thr	AAT Asn	GAT Asp	TGC Cys	CCA Pro 90	AAC Asn	TCT Ser	TCC Ser	ATA Ile	GTC Val 95	TAT Tyr	2	88
GAG	GCA	GAT	AAC	CTG	ATC	СТА	CAC	GCA	CCT	GGT	TGC	GTG	CCT	TGT	GTC	3	36

Glu	Ala	Asp	Asn 100	Leu	Ile	Leu	His	Ala 105	Pro	Gly	Cys	Val	Pro 110	Cys	Val	
ATG Met	ACA Thr	GGT Gly 115	AAT Asn	GTG Val	AGT Ser	AGA Arg	TGC Cys 120	TGG Trp	GTC Val	CAA Gln	ATT Ile	ACC Thr 125	CCT Pro	ACA Thr	CTG Leu	384
TCA Ser	GCC Ala 130	CCG Pro	AGC Ser	CTC Leu	GGA Gly	GCA Ala 135	GTC Val	ACG Thr	GCT Ala	CCT Pro	CTT Leu 140	CGG Arg	AGA Arg	GCC Ala	GTT Val	432
GAC Asp 145	TAC Tyr	CTA Leu	GCG Ala	GGA Gly	GGG Gly 150	GCT Ala	GCC Ala	CTC Leu	TGC Cys	TCC Ser 155	GCG Ala	TTA Leu	TAC Tyr	GTA Val	GGA Gly 160	480
Asp	Ala	Cys	GGG Gly	Ala 165	Leu	Phe	Leu	Val	Gly 170	Gln	Met	Phe	Thr	Tyr 175	Arg	528
CCT EPro	CGC Arg	CAG Gln	CAC His 180	GCT Ala	ACG Thr	GTG Val	CAG Gln	AAC Asn 185	TGC Cys	AAC Asn	TGT Cys	TCC Ser	ATT Ile 190	TAC Tyr	AGT Ser	576
LIGGC Cly	CAT His	GTT Val 195	ACC Thr	GGC Gly	CAC His	CGG Arg	ATG Met 200	GCA Ala	TGG Trp	GAT Asp	ATG Met	ATG Met 205	ATG Met	AAC Asn	TGG Trp	624
TAA	FAG															630
· 1																
ロ (2)	INF	ORMA'	TION	FOR	SEQ	ID 1	NO:	32:								
Addition to a second se		(i)	TION SEQU A) L B) T D) T	ENCE ENGT YPE:	CHA: H: 2: ami:	RACT 08 a no a	ERIS' mino cid	rics								
ロ (2)		(i)	SEQUI A) Li B) T	ENCE ENGT YPE: OPOL	CHA H: 2: ami: OGY:	RACT 08 a no a lin	ERIS' mino cid ear	rics								
ロ (2)	(ii	(i) ; (; (; () ) MO:	SEQUI A) Li B) T	ENCE ENGT YPE: OPOL	CHA: H: 2: ami: OGY: YPE:	RACT 08 am no a lin pro	ERIS' mino cid ear tein	rics acio	is	O: 3	2:					
(2) 	(ii (xi Gly	(i) ; (; () (i) MO:	SEQUI A) L: B) T D) T LECU	ENCE ENGT YPE: OPOL LE T	CHA: H: 2 ami: OGY: YPE:	RACT 08 am no a lin pro	ERIS' mino cid ear tein	rics acid	is ID N			Ala	Asp	Leu 15	Met	
(2) (2) Met	(ii (xi Gly	(i) :	SEQUIA) L.B) T.D) T.LECU	ENCE ENGT YPE: OPOL LE T CE D Ile 5	CHA. H: 2' ami. OGY: YPE: ESCR Asp	RACT 08 am no a lin pro IPTI Thr	ERIS' mino cid ear tein ON:	TICS acid	ID N Cys 10	Gly	Phe			12		
Met  Gly	(ii (xi Gly Tyr	(i) ; (i)	SEQUIA) LIBO TO	ENCE ENGT YPE: OPOL LE T CE D Ile 5	CHA: H: 2' ami: OGY: YPE: ESCR Asp	RACT 08 am no a lin pro IPTI Thr	ERIS' mino cid ear tein ON: Leu Gly	SEQ Thr	ID No Cys 10 Ile	Gly	Phe	·Val	Ala 30	Arg	Ala	
Met I Gly	(ii (xi Gly Tyr	(i) ; (i) (i) (i) (i) (i) (i) MO ) SE Lys Ile His 35 Leu	SEQUIA) LIBO TO	ENCE ENGT YPE: OPOL LE T CE D Ile 5 Leu Val	CHA: H: 20 ami: OGY: YPE: YPE:  Asp  Val	RACT: 08 a: no a lin pro IPTI Thr Gly Val	ERIS' mino cid ear tein ON: Leu Gly Leu 40	FICS acio SEQ Thr Pro 25 Glu	ID No Cys 10 Ile	Gly	Phe Gly Val	·Val Asn 45	Ala 30 Tyr	Arg Ala	Ala	
Met 1 Gly Leu Gly	(ii (xi Gly Tyr Ala Asn 50 Cys	(i) ; (i)	SEQUIAN LIBORY TO THE CU QUEN Val Pro 20	ENCE ENGT YPE: OPOL LE T CE D Ile 5 Leu Val	CHA: H: 2' ami: OGY: YPE: ESCR Asp Val Arg	RACT: 08 a: no a lin pro IPTI Thr Gly Val Ser 55	ERIS' mino cid ear tein ON: Leu Gly Leu 40 Phe	SEQ Thr Pro 25 Glu Ser	ID N Cys 10 Ile Asp	Gly Gly Phe	Phe Gly Val Ile 60	·Val Asn 45 Leu	Ala 30 Tyr Ala	Arg Ala Leu	Ala Thr Leu	

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Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val 135 Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly 150 145 Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg 165 170 Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp 200 195 4 4 4 4 4 5 6 (2) INFORMATION FOR SEQ ID NO: 33: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iii) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33: TGGGATATGA TGATGAACTG GTC (2) INFORMATION FOR SEQ ID NO: 34:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

<b>Q 1.1.1</b>	\															
(2)	INFO	RMAT	CION	FOR	SEQ	ID 1	10: 3	35:								
	(i)	( E ( C	A) LE B) T) C) S1	ENGTI (PE : [RANI	H: 14 nucl	CTERI 176 h Leic ESS: line	ase acio sino	pair i	:s							
	(ii)	MOI	LECUI	LE TY	PE:	CDNA	Ą									
	(iii)	HYE	POTHE	ETICA	AL: N	10										
	(iii)	ANT	TI-SE	ense :	: NO											
	(ix)	(Z	A) NA	AME/E		CDS	L473									
	(ix)	(Z	ATURE A) NA B) L(	AME/E	KEY:	mat 1	_pept L470	ide								
	(xi)	SEC	QUENC	CE DE	ESCRI	[PTIC	ON: S	SEQ ]	ID NO	): 35	5:					
TGG Trp 1	GAT Asp	ATG Met	ATG Met	ATG Met 5	AAC Asn	TGG Trp	TCG Ser	CCT Pro	ACA Thr 10	ACG Thr	GCC Ala	CTG Leu	GTG Val	GTA Val 15	TCG Ser	48
CAG _Gln																96
	TGG Trp	Gly					Leu					Met				144
	GCT Ala 50															192
	ACC Thr															240
	TCC Ser															288
	AAC Asn															336
	CTC Leu															384
AAC	TCG	TCT	GGA	TGC	CCA	GAG	CGC	TTG	GCC	AGC	TGT	CGC	TCC	ATC	GAC	432

CTATTATGGT GGTAAGCCAC AGAGCAGGAG

Asn	Ser 130	Ser	Gly	Суз	Pro	Glu 135	Arg	Leu	Ala	Ser	Cys 140	Arg	Ser	Ile	Asp	
										TAC Tyr 155						480
										GCG Ala						528
										GTG Val						576
										TTT Phe						624
AAC Asn																672
CCG Pro 225																720
■TTC □Phe																768
AAC Asn																816
FGCC Ala			GCC					GGG		TGG Trp			CCT			864
ATG Met										TAC Tyr						912
										GGG Gly 315						960
										GAG Glu						1008
										CTG Leu						1056
										CTG Leu						1104
										GAC Asp						1152

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								CTT Leu								1200
								GAC Asp								1248
								GCT Ala 425								1296
								GCC Ala								1344
TTC Phe	CTT Leu 450	GTG Val	TTC Phe	TTC Phe	TGT Cys	GCT Ala 455	GCC Ala	TGG Trp	TAC Tyr	ATC Ile	AAG Lys 460	GGC Gly	AGG Arg	CTG Leu	GTC Val	1392
CCT Pro 465																1440
CTG Leu								TAT Tyr		TAGT	TAA					1476
(2)	INFO	ORMAT	CION	FOR	SEQ	ID N	10: 3	36:								
	•	( <i>I</i>		INGTH PE:	H: 49 amir	90 an no ac	nino cid	TICS: acid								
2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		( <i>I</i> ( ) ( )	A) LE B) TY	NGTH PE:	H: 49 amir GY:	90 an no ac line	nino cid ear									
	(ii) (xi)	(A (E (E MOI SEQ	A) LE B) TY D) TO LECUI	NGTH PE: POLO E TY	H: 49 amir OGY: (PE:	90 am no ac line prot	nino cid ear cein	acio	is ID NO							
	(ii) (xi)	(A (E (E MOI SEQ	A) LE B) TY D) TO LECUI	NGTH PE: POLO E TY	H: 49 amir OGY: (PE:	90 am no ac line prot	nino cid ear cein	acio	is ID NO			Leu	Val	Val 15	Ser	
Trp	(ii) (xi) Asp	(A (E (E MOI SEQ Met	A) LE B) TY D) TO LECUI QUENO Met	INGTH (PE: )POLO LE TY CE DE Met 5	H: 49 amir OGY: PE: ESCRI	90 am no ac line prot PTIC	nino cid ear cein ON: S	acio	D NO	Thr	Ala			15		
Trp 1	(ii) (xi) Asp Leu	(A) (E) (E) MOI SEQ	A) LE B) TY D) TO LECUI QUENO Met Arg 20	INGTH (PE: )POLO LE TY CE DE Met 5	H: 49 amir OGY: PE: ESCRI Asn Pro	90 am no ac line prot  PTIC Trp  Gln	mino cid ear cein ON: S	SEQ I	D NO Thr 10 Val	Thr Asp	Ala Met	Val	Ala 30	15 Gly	Ala	
Trp 11 Gln His	(ii) (xi) Asp Leu Trp	MOI SEQ Met Leu Gly 35	A) LEB) TYD) TO LECUI QUENO Met Arg 20 Val	INGTH (PE: (POLO LE TY CE DE Met 5 Ile	H: 49 amir OGY: PE: ESCRI Asn Pro	90 am no ac line prot  PTIC  Trp  Gln  Gly	mino cid car cein ON: S Ser Ala Leu 40	SEQ Pro	ID NO Thr 10 Val Tyr	Thr Asp Tyr	Ala Met Ser	Val Met 45	Ala 30 Val	15 Gly Gly	Ala Asn	
Trp l Gln His	(ii) (xi) Asp Leu Trp Ala 50	MOI SEQ Met Leu Gly 35	A) LEB) TYD) TO LECUI QUENO Met Arg 20 Val	ENGTH (PE: (POLO LE TY CE DE Met 5 Ile Leu	H: 49 amir OGY: PE: ESCRI Asn Pro Ala Val	90 am no ac line prot  PTIC  Trp  Gln  Gly  Val 55	mino cid ear cein ON: S Ser Ala Leu 40 Met	SEQ I Pro Val 25	ID NO Thr 10 Val Tyr Leu	Thr Asp Tyr Phe	Ala Met Ser Ala 60	Val Met 45 Gly	Ala 30 Val	15 Gly Gly Asp	Ala Asn Gly	
Trp lis 65	(ii) (xi) Asp Leu Trp Ala 50 Thr	MOI SEQ Met Leu Gly 35 Lys	A) LEB) TYD) TO LECUI QUENO Met Arg 20 Val Val	ENGTH (PE: (POLO) (POLO) (PE TY) (PE DE Met (PE DE Leu) (PE Leu) (PE DE Leu) (PE DE Leu) (PE DE DE Leu) (PE DE	H: 49 amir OGY: PE: ESCRI Asn Pro Ala Val Gly 70	90 am no ac line prot  PTIC  Trp  Gln  Gly  Val 55  Gly	nino cid ear cein ON: S Ser Ala Leu 40 Met	SEQ Pro Val 25 Ala Leu	ID NOTTHE 10 Val	Thr Asp Tyr Phe Ser 75	Ala Met Ser Ala 60 Asp	Val Met 45 Gly Thr	Ala 30 Val Val	15 Gly Gly Asp Gly	Ala Asn Gly Leu 80	

Ser	Leu	Gln 115	Thr	Gly	Phe	Phe	Ala 120	Ala	Leu	Phe	Tyr	Lys 125	His	Lys	Phe
Asn	Ser 130	Ser	Gly	Cys	Pro	Glu 135	Arg	Leu	Ala	Ser	Cys 140	Arg	Ser	Ile	Asp
Lys 145	Phe	Ala	Gln	Gly	Trp 150	Gly	Pro	Leu	Thr	Tyr 155	Thr	Glu	Pro	Asn	Ser 160
Ser	Asp	Gln	Arg	Pro 165	Tyr	Cys	Trp	His	Tyr 170	Ala	Pro	Arg	Pro	Cys 175	Gly
Ile	Val	Pro	Ala 180	Ser	Gln	Val	Cys	Gly 185	Pro	Val	Tyr	Cys	Phe 190	Thr	Pro
Ser	Pro	Val 195	Val	Val	Gly	Thr	Thr 200	Asp	Arg	Phe	Gly	Val 205	Pro	Thr	Tyr
Asn I	Trp 210	Gly	Ala	Asn	Asp	Ser 215	Asp	Val	Leu	Ile	Leu 220	Asn	Asn	Thr	Arg
Pro 225	Pro	Arg	Gly	Asn	Trp 230	Phe	Gly	Cys	Thr	Trp 235	Met	Asn	Gly	Thr	Gly 240
Phe	Thr	Lys	Thr	Cys 245	Gly	Gly	Pro	Pro	Cys 250	Asn	Ile	Gly	Gly	Ala 255	Gly
≡ Asn	Asn	Thr	Leu 260	Thr	Cys	Pro	Thr	Asp 265	Суз	Phe	Arg	Lys	His 270	Pro	Glu
_ Ala	Thr	Tyr 275	Ala	Arg	Cys	Gly	Ser 280	Gly	Pro	Trp	Leu	Thr 285	Pro	Arg	Cys
_ Met	Val 290	His	Tyr	Pro	Tyr	Arg 295	Leu	Trp	His	Tyr	Pro 300	Cys	Thr	Val	Asn
Phe 305	Thr	Ile	Phe	Lys	Val 310	Arg	Met	Tyr	Val	Gly 315	Gly	Val	Glu	His	Arg 320
Phe ,	Glu	Ala	Ala	Cys 325	Asn	Trp	Thr	Arg	Gly 330	Glu	Arg	Cys	Asp	Leu 335	Glu
Asp	Arg	Asp	Arg 340	Ser	Glu	Leu	Ser	Pro 345	Leu	Leu	Leu	Ser	Thr 350	Thr	Glu
Trp	Gln	Ile 355	Leu	Pro	Cys	Ser	Phe 360	Thr	Thr	Leu	Pro	Ala 365	Leu	Ser	Thr
Gly	Leu 370	Ile	His	Leu	His	Gln 375	Asn	Ile	Val	Asp	Val 380	Gln	Tyr	Leu	Tyr
Gly 385	Val	Gly	Ser	Ala	Val 390	Val	Ser	Leu	Val	Ile 395	Lys	Trp	Glu	Tyr	Val 400
Leu	Leu	Leu	Phe	Leu 405	Leu	Leu	Ala	Asp	Ala 410	Arg	Ile	Cys	Ala	Cys 415	Leu
Trp	Met	Met	Leu 420	Leu	Ile	Ala	Gln	Ala 425	Glu	Ala	Ala	Leu	Glu 430	Asn	Leu
Val	Val	Leu	Asn	Ala	Ala	Ala	Val	Ala	Gly	Ala	His	Gly	Thr	Leu	Ser

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465	Gly	Ala	Ala	Tyr	Ala 470	Phe	Tyr	Gly	Val	Trp 475	Pro	Leu	Leu	Leu	Leu 480	
Leu	Leu	Ala	Leu	Pro 485	Pro	Arg	Ala	Tyr	Ala 490							
(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	10: 3	37:								
	(i)	(1	QUENCA) LE B) T: C) S: C) T:	engti YPE: Trani	i: 10 nucl	021 H leic ESS:	ase acio sino	pai:	cs							
]	(ii)	) MOI	LECUI	LE T	YPE:	CDNA	Ą									
:	(iii)	HY!	POTH	ETICA	AL: 1	MO										
	(iii)	) AN	ri-si	ENSE	: NO											
	(ix)	(2	ATURI A) NA B) LO	AME/			L018									
	(ix)	( 2	ATURI A) NA B) LO	AME/E				ide								
	100	950	OLIENIO	ים שי	יככסו	רסיידמ	יואר כ	:EO :	רם אוכ	٦. ٦٠	7.					
	rc co	CA CA	QUENC AA GC Ln Al	CT G1	rc Gi	rg gæ	AC AT	G G	rg go	CG GC	G GC			rp Gl		46
II GTC	CTG	CA CA co GI	- AA GO	CT G1 La Va CTC	C G1 al Va 5 GCC	rg ga al As TAC	AC AT sp Me	TCC	rg go al Al : : : :	CG GC La GI LO GTG	GG GC Ly Al	La Hi AAC	Ls Ti TGG	p Gl I GCT	Ly L5 AAG	46 94
GTC Val	CTG CTG Leu	CA CA TO GI GCG Ala	- AA GC Ln Al GGC	CTC Leu 20	TC GT al Va 5 GCC Ala	TG GA Al As TAC Tyr	AC AT Sp Me	TCC Ser	ATG Met 25	CG GC La GI LO GTG Val	GGG GGG GLY	AAC Asn GGG	TGG Trp	GCT Ala 30	AAG Lys	
GTC Val GTT Val	CTG CTG Leu	GCG Ala GTT Val	GGC Gly GTG Val	CTC Leu 20 ATG Met	TC GT al Va 5 GCC Ala CTA Leu	TAC TYT CTC Leu	AC AT TAT Tyr TTT Phe	TCC Ser  GCC Ala 40  GAT	ATG Met 25 GGC Gly	GG GC La GI LO GTG Val GTC Val	GGG GLY GAC Asp	AAC Asn GGG Gly	TGG Trp CAT His 45	GCT Ala 30 ACC Thr	AAG Lys CGC Arg	94
GTC Val GTG Val TTT	CTG CCLe Property CTG Leu TTG Leu TCA Ser	GCG Ala GTT Val GGA Gly 50 CCC	GGC Gly GTG Val 35	CT GT La Va CTC Leu 20 ATG Met GCA Ala	GCC Ala  CTA Leu  GCA Ala  GCT	TAC TAC Tyr CTC Leu GCC Ala	AC AT TAT TYr  TTT Phe  TCC Ser  55	TCC Ser  GCC Ala 40  GAT Asp	ATG Met 25 GGC Gly ACC Thr	GG GG La GI LO GTG Val GTC Val AGG Arg	GGG GGG GLY GAC Asp GGC GLY	AAC Asn GGG Gly CTT Leu 60	TGG Trp  CAT His 45  GTG Val	GCT Ala 30 ACC Thr	AAG Lys CGC Arg CTC Leu	94 142
GTC Val GTT Val GTG Val TTT Phe	TC CCLe Property of the proper	GCG Ala  GTT Val  GGA Gly 50  CCC Pro	GGC Gly GTG Val 35 GGG Gly	CTC Leu 20 ATG Met CCA Ala	GCC Ala  CTA Leu  GCA Ala  GCT Ala	TAC TYr  CTC Leu  GCC Ala  CAG Gln 70  ACT	AC AT TAT TYr  TTT Phe  TCC Ser 55  AAA Lys  GCC	TCC Ser  GCC Ala 40  GAT Asp  ATC Ile	ATG Met 25 GGC Gly ACC Thr	GG GG La G] L0  GTG Val  GTC Val  AGG Arg  CTC Leu	GGG GGC GGC GTA Val 75	AAC Asn GGG Gly CTT Leu 60 AAC Asn	TGG Trp CAT His 45 GTG Val ACC Thr	GCT Ala 30 ACC Thr TCC Ser AAC Asn CTC	AAG Lys CGC Arg CTC Leu GGC Gly	94 142 190

Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val 450 455 460

	GGG Gly															334	
	TGC Cys															382	
	GGG Gly															430	
Arg	CCC Pro 145	Tyr	Cys	Trp	His	Tyr 150	Ala	Pro	Arg	Pro	Cys 155	Gly	Ile	Val	Pro	478	
GCG Ala 160	TCT Ser	CAG Gln	GTG Val	TGC Cys	GGT Gly 165	CCA Pro	GTG Val	TAT Tyr	TGC Cys	TTC Phe 170	ACC Thr	CCG Pro	AGC Ser	CCT Pro	GTT Val 175	526	
I GTG I Val	GTG	GGG	ACG	ACC	GAT	CGG	TTT	GGT	GTC	CCC	ACG	TAT	AAC	TGG	GGG	574	
GCG Ala	AAC Asn	GAC Asp	TCG Ser 195	GAT Asp	GTG Val	CTG Leu	ATT Ile	CTC Leu 200	AAC Asn	AAC Asn	ACG Thr	CGG Arg	CCG Pro 205	CCG Pro	CGA Arg	622	
□ GGC Gly □	Asn	Trp 210	Phe	Gly	Cys	Thr	Trp 215	Met	Asn	Gly	Thr	Gly 220	Phe	Thr	Lys	670	
ACG Thr	TGT Cys 225	GGG Gly	GGC Gly	CCC Pro	CCG Pro	TGC Cys 230	AAC Asn	ATC Ile	GGG Gly	GGG Gly	GCC Ala 235	GGC Gly	AAC Asn	AAC Asn	ACC Thr	718	
	ACC Thr															766	
	AGA Arg															814	
	CCA Pro															862	
	AAG Lys															910	
	TGC Cys 305															958	
	TCA Ser															1006	
GGC	AGA	GCT	TAAT	TTA												1021	

#### Gly Arg Ala

- (2) INFORMATION FOR SEQ ID NO: 38:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 338 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe ■ Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly 100 Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg 130 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly 200 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr 215 Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu 235 Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala 250

Arg	Cys	Gly	Ser 260	Gly	Pro	Trp	Leu	Thr 265	Pro	Arg	Cys	Met	Val 270	His	Tyr	
Pro	Tyr	Arg 275	Leu	Trp	His	Tyr	Pro 280	Cys	Thr	Val	Asn	Phe 285	Thr	Ile	Phe	
Lys	Val 290	Arg	Met	Tyr	Val	Gly 295	Gly	Val	Glu	His	Arg 300	Phe	Glu	Ala	Ala	
Cys 305	Asn	Trp	Thr	Arg	Gly 310	Glu	Arg	Cys	Asp	Leu 315	Glu	Asp	Arg	Asp	Arg 320	
Ser	Glu	Leu	Ser	Pro 325	Leu	Leu	Leu	Ser	Thr 330	Thr	Glu	Trp	Gln	Ser 335	Gly	
-	Ala															
二 <u>〔</u> (2)	INF	ORMA'	rion	FOR	SEQ	ID N	10: 3	39:								
	(i	(1	QUENCA) LIB) T'C) S'D) TC	engti YPE: IRANI	H: 10 nucl	)34 k Leic ESS:	ase acio sino	pai:	cs							
ITE NAME AND ADDRESS OF THE PARTY OF THE PAR	(ii	) MO	LECU:	LE T	PE:	CDNA	Ą									
in the second	(iii	) HY	POTH	ETIC	AL: 1	10										
	(iii	) AN'	TI-S	ENSE	: NO											
	(ix	()	ATURI A) NI B) L	AME/			L032									
	(ix	(2	ATURI A) NI B) Lo	AME/I				tide								
	(xi	) SE	QUEN	CE D	ESCR.	[PTIC	ои: 3	SEQ :	ID NO	D: 39	∍:					
								IG G et Va	al Al					cp G		46
								TCC Ser								94
								GCC Ala 40								142
								GAT Asp								190

	AGC Ser 65															238
	TGG Trp															286
	GGG Gly															334
	TGC Cys															382
⊑Gln €		Trp 130	Gly	Pro	Leu	Thr	Tyr 135	Thr	Glu	Pro	Asn	Ser 140	Ser	Asp	Gln	430
AGG Arg	CCC Pro 145	TAC Tyr	TGC Cys	TGG Trp	CAC His	TAC Tyr 150	GCG Ala	CCT Pro	CGA Arg	CCG Pro	TGT Cys 155	GGT Gly	ATT Ile	GTA Val	CCC Pro	478
GCG Ala 160	TCT Ser	CAG Gln	GTG Val	TGC Cys	GGT Gly 165	CCA Pro	GTG Val	TAT Tyr	TGC Cys	TTC Phe 170	ACC Thr	CCG Pro	AGC Ser	CCT Pro	GTT Val 175	526
□GTG Val □	Val	Gly	Thr	Thr 180	Asp	Arg	Phe	Gly	Val 185	Pro	Thr	Tyr	Asn	Trp 190	Gly	574
GCG Ala	AAC Asn	GAC Asp	TCG Ser 195	GAT Asp	GTG Val	CTG Leu	ATT Ile	CTC Leu 200	AAC Asn	AAC Asn	ACG Thr	CGG Arg	CCG Pro 205	CCG Pro	CGA Arg	622
	AAC Asn															670
	TGT Cys 225															718
	ACC Thr															766
GCC	AGA Arg				GGG					CCT					CAT	814
	CCA Pro															862
	AAG Lys															910
	TGC Cys															958

305 310 315

AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GGT GAT CGA GGG
Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Gly Asp Arg Gly
320 325 330 335

CAG ACA CCA TCA CCA TCA CTA AT AG
Gln Thr Pro Ser Pro Pro Ser Leu
340

## (2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 343 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

The Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val

Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val

Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val

Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe
50 55 60

Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser 65 70 75 80

Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr 85 90 95

Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly 100 105

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln
115 120 125

Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg 130 135 140

Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala 145 150 155 160

Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val

Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala 180 185 190

Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly
195 200 205

Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala 250 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg **4**305 310 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly Gln 325 Thr Pro Ser Pro Pro Ser Leu 340 Ш (2) INFORMATION FOR SEQ ID NO: 41: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 945 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iii) ANTI-SENSE: NO (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..942 (ix) FEATURE: (A) NAME/KEY: mat\_peptide (B) LOCATION: 1..939 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41: ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCC TCC GAT 96 Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp 25

ACC Thr	AGG Arg	GGC Gly 35	CTT Leu	GTG Val	TCC Ser	CTC Leu	TTT Phe 40	AGC Ser	CCC Pro	GGG Gly	TCG Ser	GCT Ala 45	CAG Gln	AAA Lys	ATC Ile	144
CAG Gln	CTC Leu 50	GTA Val	AAC Asn	ACC Thr	AAC Asn	GGC Gly 55	AGT Ser	TGG Trp	CAC His	ATC Ile	AAC Asn 60	AGG Arg	ACT Thr	GCC Ala	CTG Leu	192
AAC Asn 65	TGC Cys	AAC Asn	GAC Asp	TCC Ser	CTC Leu 70	CAA Gln	ACA Thr	GGG Gly	TTC Phe	TTT Phe 75	GCC Ala	GCA Ala	CTA Leu	TTC Phe	TAC Tyr 80	240
AAA Lys	CAC His	AAA Lys	TTC Phe	AAC Asn 85	TCG Ser	TCT Ser	GGA Gly	TGC Cys	CCA Pro 90	GAG Glu	CGC Arg	TTG Leu	GCC Ala	AGC Ser 95	TGT Cys	288
CGC Arg	TCC Ser	ATC Ile	GAC Asp 100	AAG Lys	TTC Phe	GCT Ala	CAG Gln	GGG Gly 105	TGG Trp	GGT Gly	CCC Pro	CTC Leu	ACT Thr 110	TAC Tyr	ACT Thr	336
IGAG IGIu	CCT Pro	AAC Asn 115	AGC Ser	TCG Ser	GAC Asp	CAG Gln	AGG Arg 120	CCC Pro	TAC Tyr	TGC Cys	TGG Trp	CAC His 125	TAC Tyr	GCG Ala	CCT Pro	384
L CGA Arg	CCG Pro 130	TGT Cys	GGT Gly	ATT Ile	GTA Val	CCC Pro 135	GCG Ala	TCT Ser	CAG Gln	GTG Val	TGC Cys 140	GGT Gly	CCA Pro	GTG Val	TAT Tyr	432
TGC Cys 145	TTC Phe	ACC Thr	CCG Pro	AGC Ser	CCT Pro 150	GTT Val	GTG Val	GTG Val	GGG Gly	ACG Thr 155	ACC Thr	GAT Asp	CGG Arg	TTT Phe	GGT Gly 160	480
¶GTC □Val ⊨	CCC Pro	ACG Thr	TAT Tyr	AAC Asn 165	TGG Trp	GGG Gly	GCG Ala	AAC Asn	GAC Asp 170	TCG Ser	GAT Asp	GTG Val	CTG Leu	ATT Ile 175	CTC Leu	528
AAC Asn	AAC Asn	ACG Thr	CGG Arg 180	CCG Pro	CCG Pro	CGA Arg	GGC Gly	AAC Asn 185	TGG Trp	TTC Phe	GGC Gly	TGT Cys	ACA Thr 190	TGG Trp	ATG Met	576
AAT Asn	GGC Gly	ACT Thr 195	GGG Gly	TTC Phe	ACC Thr	AAG Lys	ACG Thr 200	TGT Cys	GGG Gly	GGC Gly	CCC Pro	CCG Pro 205	TGC Cys	AAC Asn	ATC Ile	624
					AAC Asn											672
AAG Lys 225	CAC His	CCC Pro	GAG Glu	GCC Ala	ACC Thr 230	TAC Tyr	GCC Ala	AGA Arg	TGC Cys	GGT Gly 235	TCT Ser	GGG Gly	CCC Pro	TGG Trp	CTG Leu 240	720
ACA Thr	CCT Pro	AGG Arg	TGT Cys	ATG Met 245	GTT Val	CAT His	TAC Tyr	CCA Pro	TAT Tyr 250	AGG Arg	CTC Leu	TGG Trp	CAC His	TAC Tyr 255	CCC Pro	768
TGC Cys	ACT Thr	GTC Val	AAC Asn 260	TTC Phe	ACC Thr	ATC Ile	TTC Phe	AAG Lys 265	GTT Val	AGG Arg	ATG Met	TAC Tyr	GTG Val 270	GGG Gly	GGC Gly	816
GTG	GAG	CAC	AGG	TTC	GAA	GCC	GCA	TGC	AAT	TGG	ACT	CGA	GGA	GAG	CGT	864

Val	Glu		Arg	Phe	Glu	Ala		Cys	Asn	Trp	Thr		Gly	Glu	Arg	
		275					280					285				
TGT Cys	GAC Asp 290	TTG Leu	GAG Glu	GAC Asp	AGG Arg	GAT Asp 295	AGA Arg	TCA Ser	GAG Glu	CTT Leu	AGC Ser 300	CCG Pro	CTG Leu	CTG Leu	CTG Leu	912
			GAG Glu							TAG						945
(2)	INFO	RMAT	CION	FOR	SEQ	ID N	IO: 4	12:								
	(	( <i>F</i>	SEQUE A) LE B) TY D) TO	ENGTH	H: 31 amir	.4 an	ino id									
	(ii)	MOI	LECUI	LE TY	PE:	prot	ein									
3.5. 3.0. 5.0.	•		QUENC													
Met 1	Val	Gly	Asn	Trp 5	Ala	Lys	Val	Leu	Val 10	Val	Met	Leu	Leu	Phe 15	Ala	
⊈Gly ≡	Val	Asp	Gly 20	His	Thr	Arg	Val	Ser 25	Gly	Gly	Ala	Ala	Ala 30	Ser	Asp	
Thr	Arg	Gly 35	Leu	Val	Ser	Leu	Phe 40	Ser	Pro	Gly	Ser	Ala 45	Gln	Lys	Ile	
☐ Gln	Leu 50	Val	Asn	Thr	Asn	Gly 55	Ser	Trp	His	Ile	Asn 60	Arg	Thr	Ala	Leu	
Asn 65	Суз	Asn	Asp	Ser	Leu 70	Gln	Thr	Gly	Phe	Phe 75	Ala	Ala	Leu	Phe	Tyr 80	
Lys	His	Lys	Phe	Asn 85	Ser	Ser	Gly	Cys	Pro 90	Glu	Arg	Leu	Ala	Ser 95	Cys	
Arg	Ser	Ile	Asp 100	Lys	Phe	Ala	Gln	Gly 105	Trp	Gly	Pro	Leu	Thr 110	Tyr	Thr	
Glu	Pro	Asn 115	Ser	Ser	Asp	Gln	Arg 120	Pro	Tyr	Cys	Trp	His 125	Tyr	Ala	Pro	
Arg	Pro 130	Cys	Gly	Ile	Val	Pro 135	Ala	Ser	Gln	Val	Cys 140	Gly	Pro	Val	Tyr	
Cys 145	Phe	Thr	Pro	Ser	Pro 150	Val	Val	Val	Gly	Thr 155	Thr	Asp	Arg	Phe	Gly 160	
Val	Pro	Thr	Tyr	Asn 165	Trp	Gly	Ala	Asn	Asp 170	Ser	Asp	Val	Leu	Ile 175	Leu	
Asn	Asn	Thr	Arg 180	Pro	Pro	Arg	Gly	Asn 185		Phe	Gly	Cys	Thr 190	Trp	Met	
Asn	Gly	Thr 195	Gly	Phe	Thr	Lys	Thr 200		Gly	Gly	Pro	Pro 205	Cys	Asn	Ile	

Gly	Gly 210	Ala	Gly	Asn	Asn	Thr 215	Leu	Thr	Cys	Pro	Thr 220	Asp	Cys	Phe	Arg	
Lys 225	His	Pro	Glu	Ala	Thr 230	Tyr	Ala	Arg	Cys	Gly 235	Ser	Gly	Pro	Trp	Leu 240	
Thr	Pro	Arg	Cys	Met 245	Val	His	Tyr	Pro	Tyr 250	Arg	Leu	Trp	His	Tyr 255	Pro	
Cys	Thr	Val	Asn 260	Phe	Thr	Ile	Phe	Lys 265	Val	Arg	Met	Tyr	Val 270	Gly	Gly	
Val	Glu	His 275	Arg	Phe	Glu	Ala	Ala 280	Cys	Asn	Trp	Thr	Arg 285	Gly	Glu	Arg	
Cys	Asp 290	Leu	Glu	Asp	Arg	Asp 295	Arg	Ser	Glu	Leu	Ser 300	Pro	Leu	Leu	Leu	
⊈Ser ⊈305	Thr	Thr	Glu	Trp	Gln 310	Ser	Leu	Ile	Asn							
<u>(2)</u>				FOR												
	(i)	( ) ( ) ( )	A) Li B) Ti C) Si	CE CI ENGTI YPE: TRANI OPOLO	nuci DEDNI	61 ba leic ESS:	ase p acid	pair: d	5							
	(ii)	MO!	LECUI	LE T	YPE:	CDN	F									
	(iii)	HY	POTH	ETIC	AL: 1	00/										
ļof.	(iii)	) AN	ri-si	ENSE	: NO											
	(ix)	( )		E: AME/I OCAT			958									
	(ix)	(2	ATURI A) N. B) L	E: AME/: OCAT	KEY: ION:	mat	_pep <sup>.</sup> 955	tide							•	
	(xi	) SE	QUEN	CE D	ESCR	IPTI	: NC	SEQ	ID N	0: 4	3:					
ATG Met 1	GTG Val	GGG Gly	AAC Asn	TGG Trp 5	GCT Ala	AAG Lys	GTT Val	TTG Leu	GTT Val 10	GTG Val	ATG Met	CTA Leu	CTC Leu	TTT Phe 15	GCC Ala	48
GGC Gly	GTC Val	GAC Asp	GGG Gly 20	His	ACC Thr	CGC Arg	GTG Val	TCA Ser 25	GGA Gly	GGG Gly	GCA Ala	GCA Ala	GCC Ala 30	TCC Ser	GAT Asp	96
ACC Thr	AGG Arg	GGC Gly 35	Leu	GTG Val	TCC Ser	CTC Leu	TTT Phe 40	AGC Ser	CCC Pro	GGG Gly	TCG Ser	GCT Ala 45	CAG Gln	AAA Lys	ATC Ile	144
CAG	CTC	GTA	AAC	ACC	AAC	GGC	AGT	TGG	CAC	ATC	AAC	AGG	ACT	GCC	CTG	192

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Gln	Leu 50	Val	Asn	Thr	Asn	Gly 55	Ser	Trp	His	Ile	Asn 60	Arg	Thr	Ala	Leu	
	TGC Cys															240
	CAC His															288
	TCC Ser															336
Glu	CCT Pro															384
CGA Arg	CCG Pro 130	TGT Cys	GGT Gly	ATT Ile	GTA Val	CCC Pro 135	GCG Ala	TCT Ser	CAG Gln	GTG Val	TGC Cys 140	GGT Gly	CCA Pro	GTG Val	TAT Tyr	432
TGC Cys 145	TTC Phe	ACC Thr	CCG Pro	AGC Ser	CCT Pro 150	GTT Val	GTG Val	GTG Val	GGG Gly	ACG Thr 155	ACC Thr	GAT Asp	CGG Arg	TTT Phe	GGT Gly 160	480
Val	CCC Pro	ACG Thr	TAT Tyr	AAC Asn 165	TGG Trp	GGG Gly	GCG Ala	AAC Asn	GAC Asp 170	TCG Ser	GAT Asp	GTG Val	CTG Leu	ATT Ile 175	CTC Leu	528
AAC Asn	AAC Asn	ACG Thr	CGG Arg 180	CCG Pro	CCG Pro	CGA Arg	GGC Gly	AAC Asn 185	TGG Trp	TTC Phe	GGC Gly	TGT Cys	ACA Thr 190	TGG Trp	ATG Met	576
AAT	GGC Gly															624
	GGG Gly 210															672
	CAC His															720
	CCT Pro															768
	ACT Thr															816
	GAG Glu															864
	GAC Asp															912

290 295 300

TCT ACA ACA GGT GAT CGA GGG CAG ACA CCA TCA CCA CCA TCA CTA A 958

Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu

305 310 315

TAG 961

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44: Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly 150 145 Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu 170 Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met 180 Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile 200 Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg 215

Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu

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22	25					230					235					240	
Tł	ır	Pro	Arg	Cys	Met 245	Val	His	Tyr	Pro	Tyr 250	Arg	Leu	Trp	His	Tyr 255	Pro	
C7	/S	Thr	Val	Asn 260	Phe	Thr	Ile	Phe	Lys 265	Val	Arg	Met	Tyr	Val 270	Gly	Gly	
Vá	al	Glu	His 275	Arg	Phe	Glu	Ala	Ala 280	Cys	Asn	Trp	Thr	Arg 285	Gly	Glu	Arg	
C?	/S	Asp 290	Leu	Glu	Asp	Arg	Asp 295	Arg	Ser	Glu	Leu	Ser 300	Pro	Leu	Leu	Leu	
Se 30		Thr	Thr	Gly	Asp	Arg 310	Gly	Gln	Thr	Pro	Ser 315	Pro	Pro	Ser	Leu		
(2	2)	INFO	RMAT	rion	FOR	SEQ	ID 1	NO: 4	15:								
		(i)	( <i>I</i> ( E	A) L1 B) T: C) S:	CE CH ENGTH YPE: TRANI OPOLO	H: 13 nucl	395 k Leic ESS:	ase acio sino	pai:	rs							
		(ii)	MOI	LECUI	LE TY	(PE:	CDNA	j.									
the control of the co	(	iii)	HYE	POTH	ETICA	AL: 1	40										
	(	iii)	ANT	rı-si	ENSE	: NO											
		(ix)	( Z		E: AME/I DCATI			1392									
		(ix)	( <i>F</i>		E: AME/E CCAT				cide								
,	•	(xi)	SEÇ	QUEN	CE DE	ESCRI	PTIC	on: s	SEQ 1	D NO	): 45	5:					
									GTC Val								48
									GTT Val 25								96
			Val					Arg	GTG Val				Ala				144
									TTT Phe								192
II									AGT Ser								240

	AAC Asn															288	
TAC Tyr	AAA Lys	CAC His	AAA Lys 100	TTC Phe	AAC Asn	TCG Ser	TCT Ser	GGA Gly 105	TGC Cys	CCA Pro	GAG Glu	CGC Arg	TTG Leu 110	GCC Ala	AGC Ser	336	
TGT Cys	CGC Arg	TCC Ser 115	ATC Ile	GAC Asp	AAG Lys	TTC Phe	GCT Ala 120	CAG Gln	GGG Gly	TGG Trp	GGT Gly	CCC Pro 125	CTC Leu	ACT Thr	TAC Tyr	384	
	GAG Glu 130															432	
CCT Pro 145	CGA Arg	CCG Pro	TGT Cys	GGT Gly	ATT Ile 150	GTA Val	CCC Pro	GCG Ala	TCT Ser	CAG Gln 155	GTG Val	TGC Cys	GGT Gly	CCA Pro	GTG Val 160	480	
TAT Tyr																528	
GGT Gly	GTC Val	CCC Pro	ACG Thr 180	TAT Tyr	AAC Asn	TGG Trp	GGG Gly	GCG Ala 185	AAC Asn	GAC Asp	TCG Ser	GAT Asp	GTG Val 190	CTG Leu	ATT Ile	576	
CTC Leu																624	
ATG Met																672	
	GGG Gly															720	
	AAG Lys															768	
	ACA Thr															816	
CCC Pro	TGC Cys	ACT Thr 275	GTC	AAC Asn	TTC Phe	ACC Thr	ATC Ile 280	TTC	AAG Lys	GTT Val	AGG Arg	ATG Met 285	TAC	GTG Val	GGG Gly	864	
	GTG Val 290															912	
	TGT Cys															960	
CTG	TCT	ACA	ACA	GAG	TGG	CAG	ATA	CTG	CCC	TGT	TCC	TTC	ACC	ACC	CTG	1008	

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Leu	Ser	Thr	Thr	Glu 325	Trp	Gln	Ile	Leu	Pro 330	Cys	Ser	Phe	Thr	Thr 335	Leu	
					GGC Gly											1056
GTG Val	CAA Gln	TAC Tyr 355	CTG Leu	TAC Tyr	GGT Gly	GTA Val	GGG Gly 360	TCG Ser	GCG Ala	GTT Val	GTC Val	TCC Ser 365	CTT Leu	GTC Val	ATC Ile	1104
AAA Lys	TGG Trp 370	GAG Glu	TAT Tyr	GTC Val	CTG Leu	TTG Leu 375	CTC Leu	TTC Phe	CTT Leu	CTC Leu	CTG Leu 380	GCA Ala	GAC Asp	GCG Ala	CGC Arg	1152
					TGG Trp 390											1200
GCC MAla	TTA Leu	GAG Glu	AAC Asn	CTG Leu 405	GTG Val	GTC Val	CTC Leu	AAT Asn	GCG Ala 410	GCG Ala	GCC Ala	GTG Val	GCC Ala	GGG Gly 415	GCG Ala	1248
CAT His																1296
= AAG	GGC Gly	AGG Arg 435	CTG Leu	GTC Val	CCT Pro	GGT Gly	GCG Ala 440	GCA Ala	TAC Tyr	GCC Ala	TTC Phe	TAT Tyr 445	GGC Gly	GTG Val	TGG Trp	1344
CCG UPro U															TAGTAA	1395
					-											

## (2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 463 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr
1 10 15

Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe

Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser 35 40 45

Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys 50 55 60

Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala 65 70 75 80

Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala 130 Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe 165 Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile 180 185 190 teu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn
210
220 ■ Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala

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Lys	Gly	Arg 435	Leu	Val	Pro	Gly	Ala 440	Ala	Tyr	Ala	Phe	Tyr 445	Gly	Val	Trp	
Pro	Leu 450	Leu	Leu	Leu	Leu	Leu 455	Ala	Leu	Pro	Pro	Arg 460	Ala	Tyr	Ala		
(2)	INF	ORMA'	rion	FOR	SEQ	ID N	10: 4	17:								
	(i)	(1	A) L1 B) T1 C) S1	engti Ype : Trani	i: 20 nucl	OTER 182 k Leic ESS: line	ase acio sino	pai:	rs							
	(ii)	MO1	LECUI	LE T	YPE:	CDNA	A									
	(iii)	HY	POTH:	ETICA	AL: 1	10										
A STATE OF THE STA	(iii)	AN	ri-si	ENSE	: NO											
		() () FE <i>I</i> ()	B) LO ATURI A) NA	AME/I DCATI E: AME/I	KEY:	CDS 12 mat 12	_pept	ide								
<u>.</u>																
	(xi)	SE	QUENC	CE DI	ESCRI	PTIC	on: s	SEQ 1	D NO	): 47	7:					
	(xi) TTG Leu	GGT	AAG	GTC	ATC	GAT	ACC	CTT	ACA	TGC	GGC					48
Asn 1 GTG	TTG	GGT Gly TAC	AAG Lys ATT	GTC Val 5	ATC Ile	GAT Asp GTC	ACC Thr	CTT Leu	ACA Thr 10	TGC Cys	GGC Gly GGG	Phe GGC	Ala	Asp 15 GCC	Leu AGG	48 96
Asn 1 GTG Val	TTG Leu GGG	GGT Gly TAC Tyr	AAG Lys ATT Ile 20 CAT	GTC Val 5 CCG Pro	ATC Ile CTC Leu GTC	GAT Asp GTC Val	ACC Thr GGC Gly	CTT Leu GCC Ala 25	ACA Thr 10 CCC Pro	TGC Cys CTA Leu	GGC Gly GGG Gly	Phe GGC Gly GTG	Ala GCT Ala 30 AAC	Asp 15 GCC Ala TAT	AGG Arg	
Asn 1 GTG Val GCC Ala	TTG Leu GGG Gly	GGT Gly TAC Tyr GCG Ala 35	AAG Lys ATT Ile 20 CAT His	GTC Val 5 CCG Pro GGC Gly	ATC Ile CTC Leu GTC Val	GAT Asp GTC Val CGG Arg	ACC Thr  GGC Gly  GTT Val 40 TCT	CTT Leu GCC Ala 25 CTG Leu	ACA Thr 10 CCC Pro GAG Glu	TGC Cys CTA Leu GAC Asp	GGC Gly GGG Gly GGC Gly	Phe GGC Gly GTG Val 45 CTC	Ala GCT Ala 30 AAC Asn	Asp 15 GCC Ala TAT Tyr	Leu AGG Arg GCA Ala	96
Asn 1 GTG Val GCC Ala ACA Thr	TTG Leu GGG Gly CTG Leu GGG Gly	GGT Gly TAC Tyr GCG Ala 35 AAT Asn	AAG Lys ATT Ile 20 CAT His TTG Leu	GTC Val 5 CCG Pro GGC Gly CCC Pro	ATC Ile CTC Leu GTC Val GGT Gly GTT	GAT Asp GTC Val CGG Arg TGC Cys 55	ACC Thr  GGC Gly  GTT Val 40  TCT Ser  GCT	CTT Leu  GCC Ala 25  CTG Leu  TTC Phe	ACA Thr 10 CCC Pro GAG Glu TCT Ser	TGC Cys CTA Leu GAC Asp ATC Ile	GGC Gly GGC Gly TTC Phe 60 GAA	Phe GGC Gly GTG Val 45 CTC Leu	GCT Ala 30 AAC Asn TTG Leu	Asp 15 GCC Ala TAT Tyr GCT Ala	AGG Arg GCA Ala TTG Leu GTG	96 144
Asn 1 GTG Val GCC Ala ACA Thr CTG Leu 65	TTG Leu GGG Gly CTG Leu GGG Gly 50	GGT Gly TAC Tyr GCG Ala 35 AAT Asn TGT Cys	AAG Lys ATT Ile 20 CAT His TTG Leu CTG Leu	GTC Val 5 CCG Pro GGC Gly CCC Pro ACC Thr	ATC Ile CTC Leu GTC Val GGT Gly GTT Val 70 GTC	GAT Asp GTC Val CGG Arg TGC Cys 55 CCA Pro	ACC Thr  GGC Gly  GTT Val 40  TCT Ser  GCT Ala	CTT Leu  GCC Ala 25  CTG Leu  TTC Phe  TCC Ser	ACA Thr 10 CCC Pro  GAG Glu TCT Ser GCT Ala	TGC Cys CTA Leu GAC Asp ATC Ile TAT Tyr 75	GGC Gly GGC Gly TTC Phe 60 GAA Glu	Phe GGC Gly GTG Val 45 CTC Leu GTG Val	GCT Ala 30 AAC Asn TTG Leu CGC Arg	Asp 15 GCC Ala TAT Tyr GCT Ala AAC Asn	AGG Arg GCA Ala TTG Leu GTG Val 80 GTG	96 144 192

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TAT Tyr	GAG Glu	GCA Ala	GCG Ala 100	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His 105	ACC Thr	CCC Pro	GGG Gly	TGC Cys	GTG Val 110	CCC Pro	TGC Cys	336	
GTT Val	CGG Arg	GAG Glu 115	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg 120	TGC Cys	TGG Trp	GTA Val	GCG Ala	CTC Leu 125	ACC Thr	CCC Pro	ACG Thr	384	
CTC Leu	GCA Ala 130	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser 135	GTC Val	CCC Pro	ACC Thr	ACG Thr	ACA Thr 140	ATA Ile	CGA Arg	CGC Arg	CAC His	432	
GTC Val 145	GAT Asp	TTG Leu	CTC Leu	GTT Val	GGG Gly 150	GCG Ala	GCT Ala	GCT Ala	TTC Phe	TGT Cys 155	TCC Ser	GCT Ala	ATG Met	TAC Tyr	GTG Val 160	480	
GGG Gly	GAC Asp	CTC Leu	TGC Cys	GGA Gly 165	TCT Ser	GTC Val	TTC Phe	CTC Leu	GTC Val 170	TCC Ser	CAG Gln	CTG Leu	TTC Phe	ACC Thr 175	ATC Ile	528	
TCG Ser	CCT Pro	CGC Arg	CGG Arg 180	CAT His	GAG Glu	ACG Thr	GTG Val	CAG Gln 185	GAC Asp	TGC Cys	AAT Asn	TGC Cys	TCA Ser 190	ATC Ile	TAT Tyr	576	
LCCC Pro	GGC Gly	CAC His 195	ATA Ile	ACG Thr	GGT Gly	CAC His	CGT Arg 200	ATG Met	GCT Ala	TGG Trp	GAT Asp	ATG Met 205	ATG Met	ATG Met	AAC Asn	624	
TGG Trp	TCG Ser 210	CCT Pro	ACA Thr	ACG Thr	GCC Ala	CTG Leu 215	GTG Val	GTA Val	TCG Ser	CAG Gln	CTG Leu 220	CTC Leu	CGG Arg	ATC Ile	CCA Pro	672	
CAA CGln 2225	GCT Ala	GTC Val	GTG Val	GAC Asp	ATG Met 230	GTG Val	GCG Ala	GGG Gly	GCC Ala	CAT His 235	TGG Trp	GGA Gly	GTC Val	CTG Leu	GCG Ala 240	720	
	CTC Leu															768	
GTG Vál	ATG Met	CTA Leu	CTC Leu 260	TTT Phe	GCC Ala	GGC Gly	GTC Val	GAC Asp 265	GGG Gly	CAT His	ACC Thr	CGC Arg	GTG Val 270	TCA Ser	GGA Gly	816	
GGG Gly	GCA Ala	GCA Ala 275	GCC Ala	TCC Ser	GAT Asp	ACC Thr	AGG Arg 280	GGC Gly	CTT Leu	GTG Val	TCC Ser	CTC Leu 285	TTT Phe	AGC Ser	CCC Pro	864	
GGG Gly	TCG Ser 290	GCT Ala	CAG Gln	AAA Lys	ATC Ile	CAG Gln 295	CTC Leu	GTA Val	AAC Asn	ACC Thr	AAC Asn 300	GGC Gly	AGT Ser	TGG Trp	CAC His	912	
ATC Ile 305	AAC Asn	AGG Arg	ACT Thr	GCC Ala	CTG Leu 310	AAC Asn	TGC Cys	AAC Asn	GAC Asp	TCC Ser 315	CTC Leu	CAA Gln	ACA Thr	GGG Gly	TTC Phe 320	960	
TTT Phe	GCC Ala	GCA Ala	CTA Leu	TTC Phe 325	TAC Tyr	AAA Lys	CAC His	AAA Lys	TTC Phe 330	Asn	TCG Ser	TCT Ser	GGA Gly	TGC Cys 335	CCA Pro	1008	
GAG	CGC	TTG	GCC	AGC	TGT	CGC	TCC	ATC	GAC	AAG	TTC	GCT	CAG	GGG	TGG	1056	

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Glu	Arg	Leu	Ala 340	Ser	Cys	Arg	Ser	Ile 345	Asp	Lys	Phe	Ala	Gln 350	Gly	Trp	
	CCC Pro															1104
	TGG Trp 370															1152
	TGC Cys															1200
ACG Thr	ACC Thr	GAT Asp	CGG Arg	TTT Phe 405	GGT Gly	GTC Val	CCC Pro	ACG Thr	TAT Tyr 410	AAC Asn	TGG Trp	GGG Gly	GCG Ala	AAC Asn 415	GAC Asp	1248
ITCG ISer I				ATT					CGG					AAC		1296
TTC Phe	GGC Gly	TGT Cys 435	ACA Thr	TGG Trp	ATG Met	AAT Asn	GGC Gly 440	ACT Thr	GGG Gly	TTC Phe	ACC Thr	AAG Lys 445	ACG Thr	TGT Cys	GGG Gly	1344
GGC Gly																1392
2 4 1	ACT Thr															1440
GGT	TCT Ser															1488
	CTC Leu															1536
	ATG Met															1584
	ACT Thr 530															1632
	AGC Ser															1680
	TTC Phe															1728
	AAC Asn															1776

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	TCC Ser															1824
	GCA Ala 610															1872
	CAA Gln															1920
GCC	GTG Val					-						-				1968
EAla E	GCC Ala															2016
TTC Phe	TAT Tyr	GGC Gly 675	GTG Val	TGG Trp	CCG Pro	CTG Leu	CTC Leu 680	CTG Leu	CTT Leu	CTG Leu	CTG Leu	GCC Ala 685	TTA Leu	CCA Pro	CCA Pro	2064
CGA LArg				TAGT	AA											2082
(2)	INFO	RMAT	CION	FOR	SEQ	ID N	NO: 4	18:								

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 692 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 105

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val 155 Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro T. 215 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala 225 230 235 240 Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Wal Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly 265 Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro 280 Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His 295 Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe 310 Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly 390 Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly

435 440 Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys 455 Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr 490 Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu 🖺 Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys 550 Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His 565 🖳 Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys 650 Aka Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro 680 Arg Ala Tyr Ala

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2433 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..2430 (ix) FEATURE: (A) NAME/KEY: mat peptide (B) LOCATION: 1..2427 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49: ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC 48 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT 96 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 ŸGGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG 144 🖺 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGG AGG CGA CAA CCT 192 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 🗊 ATC CCC AAG GCT CGC CGA CCC GAG GGT AGG GCC TGG GCT CAG CCC GGG 240 Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG GGG TGG GCA GGA TGG 288 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp CTC CTG TCA CCC CGC GGC TCT CGG CCT AGT TGG GGC CCT ACA GAC CCC 336 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC 384 Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys GGC TTC GCC GAC CTC GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA 432 Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu 135 GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC 480

Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp

GGC GTG AAC TAT GCA ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC

Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile

TTC CTC TTG GCT TTG CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT

Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr

170

150

528

				180					185					190			
									TAC Tyr								624
									GCG Ala								672
(									AAC Asn								720
	Ala								AGG Arg								768
	ACA								CTC Leu 265								816
									TGC Cys								864
									CGG Arg								912
U 1	AAT Asn 305	TGC Cys	TCA Ser	ATC Ile	TAT Tyr	CCC Pro 310	GGC Gly	CAC His	ATA Ile	ACG Thr	GGT Gly 315	CAC His	CGT Arg	ATG Met	GCT Ala	TGG Trp 320	960
									ACA Thr								1008
									GTG Val 345								1056
									TAC Tyr								1104
									CTC Leu								1152
1									GCC Ala								1200
									CAG Gln								1248
									ACT Thr 425								1296

							GCC Ala										1344
							CGC Arg 455										1392
							CCC Pro										1440
							TGG Trp										1488
	Val	CCC Pro	GCG Ala	TCT Ser 500	CAG Gln	GTG Val	TGC Cys	GGT Gly	CCA Pro 505	GTG Val	TAT Tyr	TGC Cys	TTC Phe	ACC Thr 510	CCG Pro	AGC Ser	1536
	Pro						ACC Thr										1584
							GAT Asp 535										1632
free:							GGC Gly										1680
Įui.	ACC						CCC Pro										1728
							ACT Thr										1776
							TCT Ser										1824
							CTC Leu 615										1872
							ATG Met										1920
							ACT Thr										1968
							AGC Ser										2016

			TTC Phe						2064
			AAC Asn 695						2112
			TCC Ser						2160
			GCA Ala						2208
ATG Met			CAA Gln						2256
GTC Val									2304
TTT Leu									2352
GGT Gly J85									2400
TTG Leu					TAGT	'AA			2433

## (2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 809 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60

Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly 65 70 75 80

-4 h-3 4 h -

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 150 Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 170 Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Ľ Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp 305 315 Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln 330 Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His 340 Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val 385 390

Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn 440 Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn 570 T Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala 580 585 Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met 600 Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe 630 Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp

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Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val 745

Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe

Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro 775

Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu 790

Leu Ala Leu Pro Pro Arg Ala Tyr Ala 805

## (2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LCCATION: 1..17
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys 10

Val

- (2) INFORMATION FOR SEQ ID NO: 52:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 22 amino acids(B) TYPE: amino acid

    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Modified-site
    - (B) LOCATION: 1..22
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:
  - Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp

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1 5 10 15

Ser Pro Thr Thr Ala Leu 20

- (2) INFORMATION FOR SEQ ID NO: 53:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

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- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1...37
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
1 10 15

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr 20 25 30

Pro Gly Cys Gly Lys 35

- (2) INFORMATION FOR SEQ ID NO: 54:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Modified-site
    - (B) LOCATION: 1..25
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr 1 5 10 15

Gln Leu Arg Arg His Ile Asp Leu Leu 20 25

- (2) INFORMATION FOR SEQ ID NO: 55:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 amino acids

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(B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1..25
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:
- Gly Gly Thr Pro Thr Leu Ala Ala Arg Asp Ala Ser Val Pro Thr Thr 1 5 10 15

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Thr Ile Arg Arg His Val Asp Leu Leu 20 25

- (2) INFORMATION FOR SEQ ID NO: 56:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:
  - Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn 1 5 10 15

Ser Thr Gly Leu

- (2) INFORMATION FOR SEQ ID NO: 57:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp Cys Pro 1 5 10 15 Asn Ser Ser Ile

(2) INFORMATION FOR SEQ ID NO: 58:

Section 1

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

Asn Val Ser

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro 1 5 10 15

Thr Val Ala Thr 20

- (2) INFORMATION FOR SEQ ID NO: 62:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr 1 5 10 15

Gln Leu Arg Arg

- (2) INFORMATION FOR SEQ ID NO: 63:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser 1 5 10 15

Ala Thr Leu Cys 20

- (2) INFORMATION FOR SEQ ID NO: 64:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64: Leu Val Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Val (2) INFORMATION FOR SEQ ID NO: 65: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65: Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Gly Cys Asn Cys Ser Ile (2) INFORMATION FOR SEQ ID NO: 66: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66: Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp (2) INFORMATION FOR SEQ ID NO: 67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single

(C) STRANDEDNESS: single

(A) LENGTH: 20 amino acids(B) TYPE: amino acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(D) TOPOLOGY: linear

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73: Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly Gln Trp His Ile Asn Ser Thr Ala Leu Asn 20 (2) INFORMATION FOR SEQ ID NO: 74: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ
Leu Asn Cys Asn Glu Ser Leu As
1 5

Ile Tyr Gln His Lys
20

(2) INFORMATION FOR SEQ ID NO: 75: (C) STRANDEDNESS: single (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74: Leu Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Trp Leu Ala Gly Leu 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75: Ala Gly Leu Ile Tyr Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu 10 15 Arg Leu Ala Ser 20 (2) INFORMATION FOR SEQ ID NO: 76: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76: Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp Gln Gly Trp Gly (2) INFORMATION FOR SEQ ID NO: 77: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77: Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser Gly Pro Asp Gln 20 (2) INFORMATION FOR SEQ ID NO: 78: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78: Ala Asn Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro Pro Lys Pro Cys (2) INFORMATION FOR SEQ ID NO: 79: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Trp His Tyr Pro Pro Lys Pro Cys Gly Ile Val Pro Ala Lys Ser Val Cys Gly Pro Val (2) INFORMATION FOR SEQ ID NO: 80: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80: Ala Lys Ser Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr 12) INFORMATION FOR SEQ ID NO: 81: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81: Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Ala Pro Thr Tyr Ser Trp Gly 20 (2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82: Gly Ala Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val Leu Asn Asn Thr 20 (2) INFORMATION FOR SEQ ID NO: 83: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid(C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83: Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser Thr Gly Phe Thr Lys Val Cys Gly Ala ☐2) INFORMATION FOR SEQ ID NO: 84: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84: Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Val Cys Ile Gly Gly Ala Gly Asn Asn Thr (2) INFORMATION FOR SEQ ID NO: 85: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Lys His Pro (2) INFORMATION FOR SEQ ID NO: 86: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86: Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly 10 Ser Gly Pro Trp INFORMATION FOR SEQ ID NO: 87: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87: Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp Tyr Pro Tyr Arg (2) INFORMATION FOR SEQ ID NO: 88: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile

(ii) MOLECULE TYPE: peptide

Ile Gly Gly Ala Gly Asn Asn Thr Leu His Cys Pro Thr Asp Cys Arg

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Ala Cys Asn Trp Thr Pro Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp

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Arg Ser Glu Leu

- (2) INFORMATION FOR SEQ ID NO: 92:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:
    - Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr Thr 10

Gln Trp Gln Val

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- I I I 12) INFORMATION FOR SEQ ID NO: 93:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:
  - Tyr Gln Val Arg Asn Ser Thr Gly Leu
  - (2) INFORMATION FOR SEQ ID NO: 94:
    - (i) SEQUENCE CHARACTERISTICS:
      - (A) LENGTH: 29 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: single
      - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (iii) HYPOTHETICAL: NO
    - (iii) ANTI-SENSE: YES
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

(2)	TMFO	RMATION FOR SEQ 1D NO: 95:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 60 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: YES	
		SEQUENCE DESCRIPTION: SEQ ID NO: 95:	
Ect L	'CCGGA	CG TGCACTAGCT CCCGTCTGTG GTAGTGGTGG TAGTGATTAT CAATTAATTG	60
重 [42]	INFO	RMATION FOR SEQ ID NO: 96:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 19 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
Mariana A	(iii)	HYPOTHETICAL: NO	
3	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 96:	
GTT	TAACC.	AC TGCATGATG	19
(2)	INFO	RMATION FOR SEQ ID NO: 97:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 97:	

GTC	CCCATC	GA GTGCGGCTAC	20
(2)	INFO	RMATION FOR SEQ ID NO: 98:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 45 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
Section 1	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 98:	
<u>_</u> _CG1		GG TACATTCCGG ACACTTGGCG CACTTCATAA GCGGA	45
型 【(2)	INFO	RMATION FOR SEQ ID NO: 99:	
		SEQUENCE CHARACTERISTICS:  (A) LENGTH: 42 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
3	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 99:	
TGC	CTCAT.	AC ACAATGGAGC TCTGGGACGA GTCGTTCGTG AC	42
(2)	INFO	RMATION FOR SEQ ID NO: 100:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 42 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 100:	

FACCCAGCA	AG CGGGAGCTCT GTTGCTCCCG AACGCAGGGC AC	42
(2) INFOR	RMATION FOR SEQ ID NO: 101:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 42 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
	SEQUENCE DESCRIPTION: SEQ ID NO: 101: IG GGGACGGAGG CCTGCCTAGC TGCGAGCGTG GG	42
<pre>2) INFOR</pre>	RMATION FOR SEQ ID NO: 102:	42
(i) (i) (i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 48 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	MOLECULE TYPE: DNA (genomic)	
(iii) (iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 102:	
CGTTATGTG	GG CCCGGGTAGA TTGAGCACTG GCAGTCCTGC ACCGTCTC	48
(2) INFOR	RMATION FOR SEQ ID NO: 103:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 42 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(iii)	ANTI-SENSE: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 103:	
CAGGGCCGT	TT CTAGGCCTCC ACTGCATCAT CATATCCCAA GC	42

(2)	INFO	RMATION FOR SEQ ID NO: 104:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 26 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 104:	
CCG	GAATG	TA CCATGTCACG AACGAC	26
_(2)	INFO	RMATION FOR SEQ ID NO: 105:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 24 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 105:	
7	CCATT	GT GTATGAGGCA GCGG	24
(2)	INFO	RMATION FOR SEQ ID NO: 106:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 23 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 106:	
GAG	GCTCCC	GC TGCTGGGTAG CGC	23
(2)	INFO	RMATION FOR SEQ ID NO: 107:	

	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 25 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
		HYPOTHETICAL: NO ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 107:	
CCT	CCGTC	CC CACCACGACA ATACG	25
(2)	INFO	RMATION FOR SEQ ID NO: 108:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
The state of the s	(ii)	MOLECULE TYPE: DNA (genomic)	
=	(iii)	HYPOTHETICAL: NO	
remarks .	(iii)	ANTI-SENSE: NO	
		SEQUENCE DESCRIPTION: SEQ ID NO: 108:	27
			<b>4</b> /
(2)	INFO	RMATION FOR SEQ ID NO: 109:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 24 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 109:	
GGA	GGCCT	AC AACGGCCCTG GTGG	24
(2)	INFO	RMATION FOR SEQ ID NO: 110:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs	

	(ii)	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 110:	
TTC	TATCG	AT TAAATAGAAT TC	22
(2)	INFO	RMATION FOR SEQ ID NO: 111:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 23 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<b>.</b>	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iii)	HYPOTHETICAL: NO	
	(iii)	ANTI-SENSE: NO	
		SEQUENCE DESCRIPTION: SEQ ID NO: 111:	
CCC	ATACGO	CT CACAGCCGAT CCC	23